

# STIC Search Report Biotech-Chem Library

#### STIO Database Technological

TO: Ruixiang Li

Location: REM/4D75/4C70

Art Unit: 1646

Friday, November 25, 2005

Case Serial Number: 09/475158

From: Toby Port

**Location: Biotech-Chem Library** 

**REM-1A59** 

Phone: 571-272-2523

toby.port@uspto.gov

#### Searen Nores

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port X22523



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From:

Li, Ruixiang

Sent:

Monday, October 31, 2005 2:39 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search of Application No.09/475,158

Please do a standard search on:

- (i).SEQ ID NOS: 3 and 5 against both commercial and interference amino acid databases;
- (ii). SEQ ID NOS: 14, 15, and 16 against both commercial and interference nucleic acid databases;
- (iii). AlaValSerGlulleGlnLeuMetHisAsnLeuGlyGlyGlyGlyGly against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li GAU 1646 REM 4D75 Mail Box 4C70 (571) 272-0875

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#\_\_\_\_\_ AA#:\_

S/L:\_\_\_ Oligomer:\_\_\_
Encode/Transl:\_
Structure #:\_\_\_\_ Text:\_
Inventor:\_\_\_ Litigation:\_\_\_

\*\*\*\*\*\*\*\*\*\*\*
Vendors and cost where applicable
STN:\_\_\_\_\_
DIALOG:\_\_\_\_
QUESTEL/ORBIT:\_\_\_\_
LEXIS/NEXIS:\_\_\_\_
SEQUENCE SYSTEM:\_\_\_\_
WWW/Internet:\_\_\_\_
Other (Specify):\_\_\_\_\_

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[Ala14]-h [Ala13]-h [Ala1, Ile [Ser14]-h [Ser13]-h [Ser13]-h [Ala14]-h Amino aci Amino aci Human par Human par

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Aar58093
Aar58103
Aar58103
Aar58108
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Aar82202
Aaw42059
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Human par Human par N-termina Human par Parathyro

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OM protein

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Sequence:

Minimum DB Maximum DB M

Database

Result

Searched:

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New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tetherl; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parathyroid hormone functional domain conjugate peptide PG5
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| /abel= PTH N-terminal_signaling_domain
/note= "resīdues 1-9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= PTH C-terminal binding portion 'note= "residues 15-31"
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                                                                                                                                                                                                                                                                                                           ALIGNMENTS
            ADQ75489
AARS8209
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AARS80030
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AARS8093
AARS8098
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                                                                                                                                                                                                                                                                                                                                                                           AAY96973 standard; peptide; 31 AA
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/label= linker
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                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-2000 (first entry)
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/label=
  (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
(JUEP/) JUEPPNER H.
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N-PSDB; AAA51729.
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AAY96973;
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Peptide
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  Aay66973 Parathyro
Aay66975 Parathyro
Aar22204 Human par
Aar74462 Parathyro
Aar768271 [Ala11]-h
Aay68015 Human mai
Aay7745 Parathyro
Aay67276 Parathyro
Aay68014 Human par
Aay68014 Human mai
Aar58026 Nalbha-m
Aar58026 Nalbha-m
Aar58026 [Ala1]-hp
Aar58026 Human par
Aar2296 Human par
Aar2296 Human par
Aay6674 Parathyro
Aay30299 Human Par
Aay3029 Parathyro
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                                                                                          ; Search time 141.5 Seconds (without alignments) 96.260 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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                                                                                             November 21, 2005, 15:52:37
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Maximum Match 100%
Listing first 45 summaries
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                         Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are namino terminal signaling functional domain of parathyroid hormone (PTH); Lis a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-14) or a PTH-related protein (PTH-rP) (1-34), R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodaling treating diseases in a mammalian call having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large mative PTH or PTHTP which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                   PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis.
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                                                                                                                                                                                             Match 100.0%; Score 160; DB 3; Length 31; Local Similarity 100.0%; Pred. No. 1.4e-14; es 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .9
/label= PTH N-terminal_signaling_domain
/note= "residues 1-9"
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/label= PTH C-terminal_binding_portion
/note= "residues 17-31"
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                                                                                                                                                                                                                                                 Location/Qualifiers
           Claim 7; Page 92-93; 119pp; English
                                                                                                                                                                                                                                                                                                         AAY96975 standard; peptide; 31 AA
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/label= linker
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N-PSDB; AAA51730.
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                                                                                                                                                                            Sequence 31 AA;
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Synthetic.
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Compounds of the structure or formula S-(L) _n-B, R_1-S-(L) _n-R or S-(L) _n-R ar an amino terminal signaling functional domain of parathyroid hormone (PTH): L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(-1,34) or a PTH-related protein (PTH-rP) (1-34); R l is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (latined). The new compound can be administered by inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rainer A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-1992;
23-DEC-1992;
23-DEC-1992;
28-JAN-1993;
14-APR-1993;
19-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUL-1993;
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AAR22294 RESULT

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veterinary medicine. These peptides may also have increased iontophoretic transdermal transport compared to wild type PTH and can be produced in high yield in recombinant E.coli. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                      Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution; osteoporosis; hypercalcaemia; hyperparathroidism; metabolic bone disease; human; veterinary medicine; iontophoretic transdermal transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New active analogues of parathyroid hormone - with increased activity, stability in serum etc., esp. for treating osteoporosis, also related DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAR74429-520 represent analogues of the 34 amino acid sequence of truncated human parathyroid hormone (PTH). These manalogues have increased activity and longer serum half life than native PTH due to eg. substitution of Met residues with Leu residues and replacing the carboxy Phe with Tyr. The carboxy terminal may also be modified by the addition of a homoserine residue or analogue, or by the addition of residues 35-84 of wild type PTH (see AAR74410). These PTH analogues may be used in the treatment of osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic bone diseases in human or account of the second of the second or analogues.
                                                                                                                                                                                                                                                                                                                                               (Hse), Hse lactone, Hse amide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.6%; Score 129; DB 2; I
80.6%; Pred. No. 2.9e-10;
ive 3; Mismatches 3;
                                                                                                                          Parathyroid hormone peptide analogue, Glyll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVSEIQLLHNGGKHLNSLERVEWLRKKLQDV
                                                                                                                                                                                                                                                                                                                                                                 residues 35-84 of PTH'
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 76; 109pp; English.
                                                                                                                                                                                                                                                                                                                                               /note= "Homoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR58271 standard; peptide; 36 AA.
AAR74462 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                /label= -H, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AFFY-) AFFYMAX TECHNOLOGIES NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US012205.
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                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Selick HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-178880/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                     recombinant E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35 AA;
                                                                                                                                                                                                                                                                                              Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oldenburg KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                         WO9511988-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                    25-MAR-2003
01-DEC-1995
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                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR58271;
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                                    AAR74462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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AAR58271
ID AAR5
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AC AAR5
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                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide(s) are parathyroid hormone derivs. - used in hormone therapy, for treating osteoporosis hyperparathyroidism and hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hPTH; protease resistant; osteoporosis; hypoparathyroidism; hypertension.
This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The peptide is an analogue of human parathyroid hormone fragment 1-34. The peptide modification defined increase resistance to proteases and therefore persistance in the blood. The peptide is used in therapy of osteoporosis, hypoparathyroidism and hypertension. The peptide may be synthesised by the Merrifield solid phase method in an automatic apparatus. See also AAR22290-99. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                     Gaps
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                                                                                                                                                 Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 129; DB 2; L. Pred. No. 2.8e-10; 1; Mismatches 4;
                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i,
                                                                                                                                               Score 133; DB 2;
Pred. No. 9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVSEIQLMHNSGKHLNSMERVEWLRKKLQDV 31
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                                                                                                                                                                                                                       1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                            SVSEIQLMHNLGGHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human parathyroid hormone 1-34 [Ser 11]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Камаве М,
                                                                                                                                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 14; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                       AAR22294 standard; peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.9%;
                                                                                                                                                 83.1%;
87.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Conservative
                                                                                                                                                                                     27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukuda T,
                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-106285/14
                                                                                                                                                 Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                          hypoparathyroidism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34 AA;
                                                                                                              Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1990;
06-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-1991;
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03-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                           AAR22294;
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Best Local &
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Gaps

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Length 35; Indels

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Matches

RESULT 5

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parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the amino terminal of PTH is important for PTH receptor binding, while the amino terminal is important for signal transduction. The present sequence is a human PTH peptide, with an amino-terminal modification which results in effective activation of the PTH-2 receptor and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteopenia, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma and a variety of cancers breast, lung and prostate carcinoma, multiple myeloma and epidermoid cancers of the head, neck and cesophagus. This peptide would be suitable for prophylaxis and treatment of the above fracture repair. The present sequence would be suitable for residue at position 1
                                                                                                                                                                                                                                                                                                                                                                New parathyroid hormone (PTH) analogs having one or more amino acid substitutions that confer PTH-1/PTH-2 receptor agonist properties, to treating old age osteoporosis and post-menopausal osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osteoporosis; agonist; PTH; human; anti-resorptive therapy; bone fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human parathyroid hormone analogue [Chall]hPTH(1-34)NH2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= OTHER
/note= "Cyclohexylalanine (Cha)"
                                  /note= "Ala is desamino residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.0%; Score 128; DB 3; Best Local Similarity 87.1%; Pred. No. 3.8e-10; Matches 27; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                           Bringhurst FR, Takasu H, Gardella TJ;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 64; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW17941 standard; peptide; 34
                                                                                                                                             99WO-US027656.
                                                                                                                                                                                  98US-0110152P
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                                                                                                                                                                                                                      (BRIN/) BRINGHURST F R.
                                                                                                                                                                                                                                        TAKASU H.
GARDELLA T J.
                                                                                                                                                                                                                                                                                                                                WPI; 2000-400045/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33 AA;
                                                                         WO200031137-A1
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Modified-site
  Key
Modified-site
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                                                                                                                                                23-NOV-1999;
                                                                                                                                                                                25-NOV-1998;
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                                                                                                           02-JUN-2000.
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(GARD/)
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ID AAW1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parathyroid hormone peptide; PTH; renal cell; osseous cell; human; signal transduction; osteoporosis; amino-terminal modification; bone disease; parathyroid hormone receptor; osteopania; hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where talcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism
                                                                         Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human amino-terminal modified parathyroid hormone analogue # 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 129; DB 2;
Pred. No. 3e-10;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waelchli R, Rainer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AVSEIQLMHGGGGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36
/note= "in amide form"
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                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                    92GB-00026415.
92GB-00026859.
92GB-00006861.
93GB-00001691.
93GB-00001692.
93GB-00001693.
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Best Local Similarity 83.9%;
Matches 26; Conservative 1
                                                                                                                                                                                                                                                                                                                                                     92GB-00015009
                                                                                                                                                                                                                                                                                                                   93GB-00014384
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    20-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis I, Schneider H,
                                      [Ala11] -hPTH (1-36) -NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-018352/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANO ) SANDOZ LTD.
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                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                 15-JUL-1992;
18-DEC-1992;
23-DEC-1992;
23-DEC-1992;
28-JAN-1993;
14-APN-1993;
14-APN-1993;
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                                                                                                                                                                                                                                                                                                                   12-JUL-1993;
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                                                                                                                                Synthetic.
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Parathyroid hormone peptide; PTH; renal call; osseous cell; human; signal transduction; osteoporosis; amino-terminal modification; bone disease; parathyroid hormone receptor; osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bis-phosphonates or calcitonin. The present sequence represents a specifically claimed peptide. NB: This sequence is not shown explicitly in the patent but was generated using the sequence of human parathyroid hormone as shown in Entrez Locus Number AAA29146
                                                                                                                                                              Parathyroid hormone analogue peptide compounds - used for stimulating bone growth, e.g. in treatment of bone fractures or osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human amino-terminal modified parathyroid hormone analogue # 5.
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Pred. No. 3.9e-10;
1; Mismatches 4.
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Best Local Similarity 83.9%;
Matches 26; Conservative
                              97US-00779768.
97US-00813534.
97WO-US022498
                                                                                                                                                                                                                Claim 6; Page; 24pp; English
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                                                                         (BIOM-) BIOMEASURE INC.
                                                                                                                                       WPI; 1998-399065/34.
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 08-DEC-1997;
                              07-JAN-1997;
07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 is cyclohexylalanine (Chal. In this example the Leu residue at position 11 of the wild-type has been substituted by Cha. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and acalitonin). N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim
                                                                                                                                                                                                                                                                                       New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and bone fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parathyroid hormone; parathormone; bone growth; bone fracture; osteroporosis; anti-resorptive therapy; calcitonin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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83.9%; Pred. No. 3.9e-10;
iive 1; Mismatches 4;
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                 /note= "In amide form"
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                                                                                                          96WO-US011292
                                                                                                                                       95US-0001105P
                                                                                                                                                   95US-0003305P.
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ses 26; Conservative
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                                                                                                            03-JUL-1996;
                                               WO9702834-A1
                                                                                                                                        13-JUL-1995;
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29-MAR-1996;
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Length 34;

AAW67276 RESULT

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/note= "N-alpha-methyl-Ala replaces wild-type Ser residue at position 1"
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                                                                                                                                                                                                                (SANO ) SANDOZ LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 AA;
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Modified-site
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28-JAN-1993;
14-APR-1993;
19-APR-1993;
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AAR58026
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                                                                                                                                                                                                                                                                                                                Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous calls, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the amino terminal is important for signal transduction. The present sequence is a human PTH speptide, with an amino-terminal modification which results in effective activation of the PTH-2 receptor and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osecoporosis, osteopeania, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma and a variety of cancers; breast, lung and prostate carcinoma, multiple myeloma and epidermoid cancers of the head, neck and oseophagus. This peptide would be suitable for prophylaxis and treatment of the above disorders. In addition, the present sequence would be suitable for residue at position 1
                                                                                                                                                                                                                                                New parathyroid hormone (PTH) analogs having one or more amino acid substitutions that confer PTH-1/PTH-2 receptor agonist properties, useful for treating old age osteoporosis and post-menopausal osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
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                                  /note= "Ala is desamino residue"
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/note= "N-Dimethyl-Ala."
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           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  Claim 3; Page 63; 69pp; English.
                                                                                                        99WO-US027656.
                                                                                                                               98US-0110152P
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                                                                                                                                                                                                   Bringhurst FR, Takasu H,
                                                                                                                                                    (BRIN/) BRINGHURST F R.
(TAKA/) TAKASU H.
(GARD/) GARDELLA T J.
                                                                                                                                                                                                                           WPI; 2000-400045/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34 AA;
                                                         WO200031137-A1
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Matches
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Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
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36
/note= "in amide form"
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92GB-00026859.
92GB-00026861.
93GB-00001691.
93GB-00001692.
93GB-00007673.
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WPI; 1994-018352/03.
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Matches 27; Conserv
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                                                                                                            Sequence 36 AA;
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28-JAN-1993;
14-APR-1993;
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23-DEC-1992;
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                                                                                                                                                    This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
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                                                                                                             New active para-thyroid hormone variants - used for treating or
                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                   Length 36;
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Pred. No. 4.1e-10;
0; Mismatches 4.
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                                                                               Waelchli R, Rainer A;
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                                                                                                                                     Example 12; Page 35; 92pp; English
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92GB-00026415.
92GB-00026859.
92GB-00026861.
93GB-00001691.
93GB-00001692.
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92GB-00026415.
92GB-00026859.
92GB-00026861.
93GB-0001691.
93GB-00001692.
93GB-00001693.
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1 Similarity 87.1%;
27; Conservative (
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                                                                               Schneider H,
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                                                                                              WPI; 1994-018352/03
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Best Local Similarity
                                                               (SANO ) SANDOZ LTD
                                                                                                                                                                                      hypoparathyroidism
                                                                                                                                                                                                     Sequence 36 AA;
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                               28-JAN-1993;
14-APR-1993;
19-APR-1993;
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18-DEC-1992;
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28-JAN-1993;
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 18-DEC-1992;
23-DEC-1992;
                         28-JAN-1993
                23-DEC-1992
                                                                                                                      preventing
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/note= "N-alpha-methyl-Ala replaces wild-type Ser residue
at position 1"
                                                                                                            This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
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New active para-thyroid hormone variants - used for treating preventing osteoporosis etc.
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Pred. No. 4.1e-10;
0; Mismatches 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rainer
                                                                                                                                                                                                                                                                                                                                                                               31
                                                                                                                                                                                                                                                                                                                                                                                                   New active para-thyroid hormone variants preventing osteoporosis etc.
                                                                                                                                                                                                                                                                                                                                                                               1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waelchli R,
                                                                        Example 260; Page 46; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 34; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR58019 standard; peptide; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92GB-00015009.
92GB-00026415.
92GB-00026819.
92GB-0001691.
93GB-00001692.
                                                                                                                                                                                                                                                                                         80.0%;
87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93GB-00014384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-018352/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tetherl; osteoporosis.
                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parathyroid hormone functional domain conjugate peptide PG9.
                                                                                                                                                                                       Length 38;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .5
/label= PTH N-terminal_signaling_domain
/note= "residues 1-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= PTH C-terminal binding_portion
/note= "residues 15-31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potts JT, Jueppner H;
                                                                                                                                                                                    Match 80.0%; Score 128; DB 2; L. Local Similarity 87.1%; Pred. No. 4.4e-10; e8 27; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY96974 standard; peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 93; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .14
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gardella TJ, Kronenberg HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US031108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0114577P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2000 (first entry)
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/label= I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
(JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-452384/39.
N-PSDB; AAA51731.
                                                                                                                                   Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200039278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96974;
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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Matches
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TANY 96974
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CC reformation, bone resorption and/or bone remodeling, treating diseases

C and disorders associated with decreased tetheria cativity, increasing cAMP

CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or

CC inhalation unlike the large native PTH or PTHTP which avoids the need for

CC inhalation unlike the large native PTH or PTHTP which avoids the need for

CC regular injections to treat osteoporosis

XX

Sequence 31 AA;

Query Match

Best Local Similarity 87.1%; Score 127; DB 3; Length 31;

Best Local Similarity 87.1%; Prec. NO. 4.8e-10;

Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

1 AVSEIGLANGGGGGGGLNSMERVEWLRKKLQDV 31

Db

1 AVSEIGLANGGGGGGGLNSMERVEWLRKKLQDV 31

Search completed: November 21, 2005, 16:10:11

Job Line: 142.5 secs
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Fri Nov 25 10:36:41 2005

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                    Copyright
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sw model protein search, using OM protein November 21, 2005, 16:05:13 Run on:

; Search time 23.5 Seconds {without alignments} 126.924 Million cell updates/sec

1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31 US-09-475-158A-3 160 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seq. Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* 1: Dir1:\* 2: Dir2:\* 3: Dir3:\* 4: Dir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	2	parathyroid hormon	choline O-acetyltr	choline O-acetyltr	carnitine O-acetyl	probable receptor	PTS lichenan-speci	sigma 1 protein -	sigma 1 protein -	carnitine acetyltr	choline O-acetyltr	choline O-acetyltr		hypothetical prote	carnitine O-acetyl		hypothetical prote	kinesin homolog KH	L-ascorbate peroxi	ಹ	moaD protein (impo	hypothetical prote	DNA-directed RNA p	mevalonate kinase					
ΩI	PTHU	PTBO	PTPG	JC4202	A05091	151851	A34937	B43777	A48319	A55720	T03784	D69651	HMXRH2	C34829	S52782	: A39961	2 A60202	S74845		2 S53369	S62572		. A53939	H	139767	2 T45539	H	: F82336	BVBYR1
Length DB	115 1	115 1	115 1	115 2	115 2	105 2	119 2	641 2	644 2	626 2	990	110 2	399 1	462 2	627 2	•••	748 2	463 1	•	627 2				421 2		588 2	319 2	1375 2	443 1
Query Match	78.1	74.4	73.1	72.5	68.8	65.6	53.1	38.8	38.8	37.5	36.9	35.6	35.0	35.0	35.0	35.0	35.0	34.4	34.4	33.8	33.1	32.5	32.5	32.2	31.9	31.9	31.6	31.6	31.2
Score	125	119	117	116	110	105	82	62	62	9	29	57	26	26	96	26	26	55	55	54	53	52	52	51.5	51	51	50.5	ö	20
Result No.	-	7	٣	4	S	9	7	80	Ø.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

retinoblastoma bin	hypothetical prote	hypothetical prote	pur operon repress	activator of purin	acetyl xylan ester	probable DNA bindi	choline O-acetyltr	choline O-acetyltr	hypothetical prote	virulence-associat	virulence associat	parathyroid hormon	_	MgPa operon hypoth	amidase (EC 3.5.1.
158383	T00637	H83405	E95231	G98095	E72421	T03605	A36526	A24889	T45997	T09450	C64559	S10202	G72698	A64221	C42725
Н	7	~	N	~	N	~	~	N	~	2	7	-	~	Н	7
1257	1922	158	275	275	325	425	720	728	219	94	94	176	301	361	206
31.2	31.2	30.9	30.9	30.9	30.6	30.6	30.6	30.6	30.3	30.0	30.0	30.0	30.0	30.0	30.0
20	20	49.5	49.5	49.5	49	49	49	49	48.5	48	48	48	48	48	48
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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parachyroid hormone precursor [validated] - human
NyAlternate names: proparathyroid hormone
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence\_revision 19-Jan-1996 #text\_change 09-Jul-2004
C;Accession: A19399, S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410; I38
R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.E.; Preeman, M.W.; Pennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.T.; Preeman, M.W.; Pennick, B.J.; Hendy, G.N.; Potts Jr., J
R;Vasicek, T.J.; McDevitt, B.J.; Preeman, B.J.; P

A; Molecule type: DNA

A;Residues: 1-115 <VAS>
A;Residues: 1-115 <VAS>
A;Cross-references: UNIPROT: P01270; UNIPARC: UPI000013290A; GB:J00301; NID:g190702; PIDN: R;Yamaguchi, T.; Fukase, M.; Sugimoco, T.; Kido, H.; Chihara, K.
Biol. Chem. Hoppe-Seyler 375, 821-824, 1994
A;Title: Purification of meprin from human kidney and its role in parathyroid hormone dè A;Reference number: S53790; MUID:95225988; PMID:7710697

A; Accession: S53790

A; Modecule type: protein
A; Residues: 'X',33-46;65-84;105-110 <YAM>
A; Residues: 'X',33-46;65-84;105-110 <YAM>
A; Residues: 'X',33-46;65-84;105-110 <YAM>
A; Residues: 'X',33-46;65-84;105-110 over the control of the

A;Molecule type: protein A;Molecule type: protein A;Residues: 26-37 cJAC-A;Cross-references: UNIPARC:UP100001734E4 A;Cross-references: UNIPARC:UP100001734E4 B;Oletad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.1 Eur. J. Blochem. 205, 311-319, 1992

A, Title: Isolation and characterization of two biologically active O-glycosylated forms

ation. A;Reference number: S21199; MUID:92209518; PMID:1555591

A; Accession: S21199

A,Molecule type: protein A,Residues: 32-114,'N' <OLS> A,Cross-references: UNIPARC:UP100001734ES

A;Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation, R;Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L.H P.C.; Mall, A.G., Sch. US.A. T., 384-388, 1974
A;Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid A;Reference number: A93789; MUID:74111656; PMID:4521809

A;Molecule type: protein A;Residues: 32-68 <NIA> A;Cross-references: UNIPARC:UP1000002DA05 R;Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D. Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

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PRESON YOUGH MATCHES PROCURED. - DAYLOR GENERAL MS. 1, 18695, 144996, A01524
C. Cheresian, 249499, A01921 Matches and Control of the Control 
                                                32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62
                                                                                                                                                                         RESULT 2
PTBO
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A,Title: Human parathyroid hormone; amino-acid sequence of the amino-terminal residues 1 A,Febidenal type: protein
A,Moceania (1973) and 33733, MAID-130022; PRID 450319
A,Moceania (1973) and 33733, MAID-130022; PRID 450319
A,Moceania (1973) and 33733, MAID-130020, PRID 450319
A,Moceania (1973) and 470020
A,Moceania (1973) and 470000017455
B,Moceania (1973) and 470000017455
B,Moceania (1973) and 470000017455
B,Moceania (1973) and 17714516; PRID: 1125201
A,Moceania (1973) and 17714516; PRID: 1125201
A,Moceania (1973) and 17714516; PRID: 1125201
B,Moceania (1973) and 17714516; PRID: 1771416; PRID: 1771416
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Pred. No. 1.9e-09;
1; Mismatches 4; Indels
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83.9%;
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Gaps

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A,Cross-references: UNIPROT:P52212; UNIPARC:UP10000132908; GB:U15662; NID:g558915; PIDN: C;Superfamily: parathyroid hormone; parathyroid hormone homology C;Keywords: hormone P;1-31/Domain: signal sequence #status predicted <SIG>P;1-31/Domain: parathyroid hormone homology <PTH>P;30-64/Domain: parathyroid hormone homology <PTH>P;310-64/Domain: parathyroid hormone #status predicted <MAT>
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A.Accession: ACOS.
A.Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein and A;Reference number: JC4201, MUID:95369696; PMID:7642102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Accession: JC4202
R;Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.C.
Gene 160, 241-243, 1995
A;Title: Sequences of the CDNAs encoding canine parathyroid hormone-related protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parathyroid hormone precursor - rat
Cispecies: Rattus norvegiums (Norway rat)
Cibace: 05-Jun.1987 #sequence_revision 05-Jun.1987 #text_change 09-Jul-2004
Cibacession: A05091; A26806
Rijeainich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
Rijeainich, G.; Kronenberg, H.B.; Potts Jr., J.T.; Habener, J.F.
A; Reference number: A05091; MUID:84135846; PMID:6321505
                                                                                                                                                                                                                                                                                                                                                                    parathyroid hormone precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 1.8e-07;
3; Mismatches 5; Indele
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Pred. No. 2.9e-08;
2; Mismatches 5; Indels
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C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;30-64/Domain: parathyroid hormone homology <PTH>
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A;Residues: 1-115 <SCH>
    Indels
        4
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3; Mismatches
        3, Mismatches
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                                                                                     1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV
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74.2%;
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Best Local Similarity 77.44
Matches 24, Conservative
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Matches 23; Conservative
        Conservative
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A; Residues: 1-115 <ROS>
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        24;
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: B26806; A90390; A90376; A01535
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nuclectide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: B26806
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Reference number: A26805; UNIPARC:UPIO00013290B; GB:X05722; GB:Y00409; NID:g18
R;Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
Blochemistry 14, 361-3652, 1975
A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial aminc
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Residues: 26-115 < CHU>
A;Cross-references: UNIPARC:UPI00001592DF
A;Cross-reference number: A90390; MUID:74253317; PMID:4840833
A;Reference number: A90376; MUID:74253317; PMID:4840833
A;Reference number: A90376; MUID:74253317; PMID:4840833
A;Reference number: A90376; MUID:74253317; PMID:4840833
Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: 145976; MUID:83105964; PMID:6185374
A;Accession: 145976; MUID:83105964; PMID:6185374
A;Accession: 145976; MUID:83105964; PMID:6185374
A;Accession: 145976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-115 <WE3>
A;Residues: 1-115 <WE3>
A;Cross-references: UNIPARC:UPI0000132907; GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:
C;Genetics:
A;Gene: PTH
A;Introns: 29/2
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-115/Product: proparathyroid hormone #status experimental <PMAT>
F;26-31/Domain: propeptide #status experimental <PMAT>
F;30-64/Domain: parathyroid hormone homology <PTH>
F;32-115/Product: parathyroid hormone #status experimental <WAT>
F;32-115/Product: parathyroid hormone #status experimental <WAT>
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A,Accession: A90376
A,Molecule type: protein
A,Residues: 32-109 c&AUs
A,COSB-references: UNIPARC:UPI00001734E0
A,CrosB-references: UNIPARC:UPI00001734E0
A,CrosB-references: UNIPARC:UPI00001734E0
A, J. Med. 56, 759-766, 1974
A,Title: Recent studies on the chemistry of human, bowine and porcine parathyroid hormon
A,Reference number: A90030; MUID:74173303; PMID:4598526
A,Contents: annotation
C,Superfamily: parathyroid hormone; parathyroid hormone homology
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;30-64/Domain: parathyroid hormone homology <PTH>
;32-115/Product: parathyroid hormone #status experimental <MAT>
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Pred. No. 1.2e-08;
1; Mismatches 5; Indels
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Best Local Similarity 80.6'
Matches 25; Conservative
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Best Local Similarity
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C. Species: Rattus forzae (BC 2.1.6) - rat
C. Species: Rattus forzae (BC 2.1.6) - rat
C. Species: Rattus norvegicus (Norway rat)
C. Species: Rattus norvegicus (Norway rat)
C. Accession: A4019; A43777; A40801; A5670
C. Accession: A4010; A43777; A40801; A5670
C. Accession: A4010; A3777; A40801; A5670
C. A. Serverad S.; Faynadd, B.; Ansieau, S.; Coppola, T.; Weber, M.J.; Mallet, J.
U. Neurosci. Res. 23, 266-273, 1908
A.; Title: Complete sequence of a cDNA encoding an active rat choline acetyltransferase: a
A. Accession: A4010
A. Stetus: preliminary; not compared with conceptual translation
A. Stetus: preliminary; not compared with conceptual translation
A. Residues: UNPROT: P2729; UNIPARC: UP1000017535A
A. Cross reference: UNPROT: P2729; UNIPARC: UP100017535A
B. Islai, K.; Oda Y.; Ichkava, T.; Deguchi, T.
A. Reference number: A41777; MUID: 90251122; PMID: 2160042
A. Reference number: A43777; MUID: 916485; PMID: 831893
A. A. Reference number: A49881; MUID: 916485; PMID: 831893
A. A. Reference number: A49881; MUID: 916485; PMID: 841888
A. Reference number: A49881; MUID: 91240983; PMID: 8479291
A. Reference number: A56876; MUID: 92240983; PMID: 8479291
A. Reference number: A56876; MUID: 92240983; PMID: 8479291
A. Reference number: A56876; MUID: 92240983; PMID: 8479291
R; Ishii, K.; Oda, Y.; Ichikawa, T.; Deguchi, T.

Brain Res. Mol. Brain Res. 7 151-159 1990

A; Title: Complementary DNAs for choline acctyltransferase from spinal cords of rat and mc A; Reference number: A43777; MUID:90251122; PMID:2160042

A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-641 < ISHA
A; Residues: 1-641 < ISHA
A; Cross-references: UNIPROT:003059; UNIPARC:UPI000017535E
B; Miaawa, H.; Ishii, K.; Deguchi, T.
J; Biol. Chem. 267, 20399, 1992
A; Title: Gene expression of mouse choline acetyltransferase. Alternative splicing and ide
A; Reference number: A44023; MUID:93015919; PMID:1400357
A; Accession: A44023; MUID:93015919; PMID:1400357
A; Accession: A44023
A; Residues: 1-219 < MIS>
A; Cross-references: UNIPARC:UPI000016CC80; GB:D12487; NID:9220366; PIDN:BAA02056.1; PID:g:
A; Cross-reference extracted from NCBI backbone (NCBIP:115801)
C; Superfamily: carnitine O-acetyltransferase
C; Reywords: acyltransferase; coenzyme A
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38.8%; Score 62; DB 2; Length 641;
Best Local Similarity 51.9%; Pred. No. 2.3;
Matches 14; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 LQLLHGGGCSLNGANR--WYDKSLQFV 322
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PA4977

PA497

PA497
                                                                                                               Justify to the fragment)

Justify and hormone - rat (fragment)

Cispecies: Rattus norvegicus (Norway rat)

Cispecies: Rattus norvegicus (Norway rat)

Cispecies: Rattus norvegicus

Cispecies: Accession: 151851

Rischmelzer, H. 1. 21, 228-229, 1984

Ay: General Technol. 21, 228-229, 1984

Ay: Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone. Ay: Reference number: 151851

Aycession: 151861

Aycession: 151861

Aycession: 151881

Aymolecule type: mRNA

Ayelecule type: mRNA

Cisconetics:
Cisconetics: PTH

Cisconet
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C:Species: Mus musculus (house mouse)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accesion: B43777; A44023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 21
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R;Xu, Y:; Zhu, Q:; Lamb, C.
submitted to the EMBL Data Library, June 1995
A;Description: Molecular cloning and characterization of a rice gene encoding leucine-rl,
A;Reference number: Z15083
A;Accession: T03784
A;Accession: T03784
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-990 <XUY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 31-Dec-2004
C;Accession: D69651; S5761
C;Accession: D7, Bruschi, C.V.; Eddwell, B.; Capbret, C.; Ferrari, E.
Nature 390, 249-255, 1997
C;Bruschi, C.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler.
A;Authors: Lauber, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, B.; Hullo, M.F.
Kecter, P.; Koningstein, G.; Krodph, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadah, Y.; Sacho, T. M.; Sentonin,
A;Authors: Schleich, S.; Schroeter, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
A;Authors: Yoshikawa, H.F.; Zumanco, H.; Yamane, K.; Yasaumoco, K.; Yata, K.; Yoshida, K.;
A;Atthors: Yoshikawa, H.F.; Zumetelin, E.; Yoshikawa, H.; Danchin, A.; Atthors: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT:P46319; UNIPARC:UP1000060C4F; GB:Z99123; GB:AL009126; NID:ġ
Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 870/1
C;Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.cross-references: UNIPROT:040699; UNIPARC:UP100000A9030; EMBL:X89226; NID:g1263159; Pt
A.Experimental source: cv. IR36, leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Superfamily: phosphotransferase system, lactose/cellobiose-specific component IIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTS lichenan-specific enzyme IIA component licA - Bacillus subtilis N;Alternate names: probable cellobiose phosphotransferase enzyme III C;Species: Bacillus subtilis
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Pred. No. 8.9;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             625 MRGGGGGAGSQLRLRWDSKKM 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.4%;
Matches 11; Conservative
                                      receptor protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                              C, Accession: T03784
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A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: 1rk2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetica
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A;Cross-references: UNIPARC:UPI0000175360; EMBL:X79827
A;Experimental source: clone SM-1400
C;Genetics:
A;Gene: GDB:CRAT; CAT1
A;Cross-references: GDB:359759; OMIM:600184
A;Map position: 9934.1-9934.1
A;Mote: at least one intron occurs before the initiator of the peroxisomal form
C;Superfamily: carnitine O-acetyltransferase precursor, mitochondrion; peroxisome
C;Keywords: acyltransferase; alternative splicing; coenzyme A; mitochondrion; peroxisome
C;Keywords: acyltransferase precursor, mitochondrial splice form #stat
F;1-28/Domain: transit peptide (mitochondrion) #status predicted <nmp>F;22-626/Product: carnitine O-acetyltransferase, peroxisomal splice form #stat
F;29-626/Product: carnitine O-acetyltransferase, mitochondrial #status predicted <MATM>F;30-626/Region: peroxisome/glyoxysome location signal #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
A55720
acantitine O-acetyltransferase (EC 2.3.1.7) precursor, mitochondrial - human
NyAlternate names: catl protein
NyContains: carnitine O-acetyltransferase, peroxisomal
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A55720, S50030; S50029
R;Corti, O.; Finocchiaro, G.; Rossi, E.; Zuffardi, O.; Dibonato, S.
Genomics 23, 94-99, 1994
A;Title: Molecular cloning of CDNAs encoding human carnitine acetyltransferase and mappi
A;Reference number: A55720, MUID:95130117; PMID:7829107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricorti, O.; Dibonato, S.; Finocchiaro, G.
Biochem. J. 303, 37-41, 1994
A;Title: Divergent sequences in the 5' region of cDNA suggest alternative splicing as
A;Reference number: $50029; MUID:95031982; PMID:7945262
                                                                                                                                                                                                                                                                                                 1,
                                      A;Experimental source: spinal cord
A;Experimental source: spinal cord
A;Note: sequence extracted from NCBI backbone (NCBIN:130081, NCBIP:130082)
C;Superfamily: carnitine O-aceryltransferase
C;Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                                 Gaps
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A;Molecule type: mRND
A;Residues: 22-626 - CCO2>
A;Cross-references: UNIPROT:P43155; UNIPARC:UP1000002A53F; EMBL:X78706
                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                           Length 644
                                                                                                                                                                                                                                                                                                 9; Indels
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                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                           Query Match
38.8%; Score 62; DB
Best Local Similarity 51.9%; Pred. No. 2.3;
Matches 14; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           297 LÓLLHGGGCSLNGANR--WYDKSLÓFV 321
                                                                                                                                                                                                                                                                                                                                                                          5 IQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-52 <COR>
A;Crosa-references: UNIPARC:UPI00017535F;
A;Experimental source: clone SM-1200
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A; Cross-references: UNIPARC: UPI000017535D
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A; Residues: 22-52 < CO3 >
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DB 2; Length 110;

35.6%; Score 57;

Query Match

RESULT 11

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Gaps

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C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S22782
R;Brunner. S.; Kramar, K.; Hofbauer, R.
submitted to the EMBL Data Library, March 1995
A;Pescription: A novel cell cycle regulated carnitine acetyltransferase in S3T3 cells.
A;Reference number: S52782
A;Accession: S2782
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QLMHGGGGGLNSMERVEWLRKKLQ 29
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C34829

Signal 1 protein - reovirus type 2 (strain Jones)

NyAlternate names: hemagglutinin; minor outer capsid protein
C;Species: reovirus type 2

A;Note: nose Hemo sapiens (man)
C;Date: nose Hemo sapiens (man)
C;Date: nose Hemo sapiens (man)
C;Date: nose Hemo sapiens
C;Accession: C34829
A;Nibert, M.L.; Dermody, T.S.; Fields, B.N.
J. Virol. 64, 2976-2288, 1990
A;Title: Structure of the reovirus cell-attachment protein: a model for the domain organ
A;Reference number: A34829
A;Reference number: A34829; MUID:90244415; PMID:2335823
A;Retus: prellminary
A;Rocession: C34829
A;Retus: prellminary
A;Rocession: C34829
A;Retus: prellminary
A;Retus: new I-462 < NIB>
C;Genetics:
C;Genetics:
C;Superfamily: reovirus sigma 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anyternet names: hemagglutinin

Cispecies: recovirus type 2

NiAlternete names: hemagglutinin

Cispecies: recovirus type 2

A;Note: host Homo sapiens (man)

Cispecies: recovirus type 2

A;Note: host Homo sapiens (man)

Cispecies: recovirus type 2

A;Note: host Homo sapiens (man)

Cispecies: recovirus type 2

A;Note: host Homo sapiens (man)

Cispecies: A; Cimelo, R.A.; Wiener, J.R.; Joklik, W.K.

R;Cashdollar, L.W.; Cimelo, R.A.; Wiener, J.R.; Joklik, W.K.

R;Cashdollar, L.W.; Cimelo, R.A.; Wiener, J.R.; Joklik, W.K.

A;Reference number: A94035; MUID:85113159; PMID:3855545

A;Reference number: A94035; MUID:85113159; PMID:3855545

A;Residues: L.399 c.As.

A;Residues: L.399 c.As.

A;Residues: L.399 c.As.

A;Cross-references: UNIPROT:P04507; UNIPARC:UPI0000163913; GB:MI0261; NID:9808813; PIDN:
C;Genetics: S1; sigma 1

C;Superfeanily: recovirus sigma 1 protein

C;Reywords: glycoprotein; hemagglutinin

C;Reywords: glycoprotein; hemagglutinin

C;Reywords: glycoprotein; hemagglutinin

F;237,243,297/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                          Gaps
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                                    Best Local Similarity 40.6%; Fred. No. 1.7; Matches 13; Conservative 5; Mismatches
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RESULT 15 852782 852781 852781 acetyltransferase - mouse C;Species: Mus musculus (house mouse)

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November 21, 2005, 15:55:27; Search time 146.5 Seconds (without alignments) 149.293 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                 sw model
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Gapop 10.0 , Gapext 0.5
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160
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Perfect score:
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2166443 Total number of hits satisfying chosen parameters:

residues

2166443 seqs, 705528306

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

summaries UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 su Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	P01270 homo sapien	Q9xt35 macaca fasc	Q4vb48 homo sapien	Q9nlv0 equus cabal	8 pos		P52212 canis famil	Q80wz2 rattus norv	rattu	Q9g167 felis silve		P15743 gallus gall			Q9i8e9 fugu rubrip		_	Q6wq24 brachydanio	Q9i8u2 sparus aura	Q5nzf6 azoarcus sp	Q8bqn4 mus musculu	rat	_	_	_	_	Q4tgy4 tetraodon n		homo	2 homo s	Q40699 oryza sativ
SUMMERS		D	PTHY HUMAN	PTHY MACFA	Q4VB48 HUMAN	Q9N1V0 HORSE	PTHY BOVIN	PTHY_PIG	PTHY CANFA	Q80WZ2 RAT	PTHY RAT	PTHY_FELCA	O9Z0L6 MOUSE	PTHY CHICK	Q6W9J4_FUGRU	CB30 HYDMC	Q918E9 FUGRU	Q6H9R6_PLAFE	Q531Q0_PLAFE	Q6WQ24_BRARE	Q918U2_SPAAU	BIOH AZOSE	Q8BQN4 MOUSE	CLAT RAT	CLAT MOUSE	Q8BQV2_MOUSE	QSTLZ1_BRARE	Q6WQ25_BRARE	Q4TGY4 TETNG	Q4SRM4_TETNG	CACP HUMAN	QST952 HUMAN	Q40699_ORYSA
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	Query	Match	78.1	78.1	78.1	75.6	74.4	73.1	72.5	68.89	68.8	68.1	67.5	53.1	42.5	40.6	40.6	39.4	39.4	38.8	38.8	38.8	38.8	38.8	38.8	38.8	•	37.5	37.5	37.5	37.5	37.5	36.9
		Score	125	125	125	121	119	117	116	110	110	109	108	85	68	65	65	63	63	62	62	62	62	62	62	62	9	9	9	9	9		29
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Q4rsf3 tetraodon n Q91y91 peromyscus Q91y91 peromyscus Q91y91 peromyscus P46319 bacillus su Q6ft33 candida gla Q463m6 azotobacter Q642h6 brachydanio Q529n5 oryza sativ Q8b35 oryza sativ Q8b35 oryza sativ Q8b35 oryza sativ Q8b35 brachydanio Q96658 oryza sativ Q58px3 brachydanio Q4vva3 brachydanio
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177 31 31 110 208 549 631 994 1449 1249 198 198
5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

# ALIGNMENTS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE 3169834; PubMed=6220408;
Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J., Hendy G.N., Vasicek T.J., Rich A., Kronenberg H.M.;
Potts J.T. Jr., Rich A., Kronenberg H.H.M.;
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MEDLINE=74111656; PubMed=4521809;
Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
Niall H.D., Sauer R.T., Darobsh G.D., Potts J.T. Jr.;
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MEDLINE=44174967; PubMed-4833516;
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                                                        21-JUL-1986 (Rel. 01, Created)
113-AUG-1987 (Rel. 05, Last sequence update)
13-SBP-2005 (Rel. 48, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE OF 26-40.
PubMed=15340161; DOI=10.1110/ps.04682504;
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PROTEIN SEQUENCE OF 61-83 AND 84-115.
MEDIINE=79082855; PubMed=728431;
Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,
                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).
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                           115 AA.
                           PRT;
                            STANDARD;
                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parathyroid hormone.
                                                                                                                                                                                  Homo.
NCBI_TaxID=9606;
                            PTHY HUMAN
                                                                                                                          Name=PTH
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RESULT 1
PTHY HUMAN
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PROSITE; PS00335; PARA
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SIGNAL
PROPEP
  TRUCTURE BY NMR OF 32-65.

MEDLINE=2129748; PubMed=2069952;

MINESLOP9748; PubMed=2069952;

MINESLIGATION T., Wray V., Schomburg D., Wingender E., Mayer H.;

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MEDLINE-ZOOGG19; PUBMEd=10623601; DOI=10.1006/bbrc.1999.1958;
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MEDIATNE=79146516; PubMed=1125201;
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STRUCTURE BY NWR OF 32-68.
STRUCTURE BY NWR OF 32-68.
MEDLINE-95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;
Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
Roesch P.;
                                                                                    Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N., O'Riordan J.L.H., Potts J.T. Jr.; (In) Talmadge R.V., Owen M., Parsons J.A. (eds.); Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation, Amsterdam (1975).
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Barden J.A., Cuthbertson R.M.;
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WARIANT FIH ARG-18.
WEDLINE-91009911; PubMed=2212001;
Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
Arnold A., Horst S.A., Gardella F.J., Baba H., Levine M.A.,
Kronenberg H.M.;
Kronenberg H.M.;
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MDDLINE=7327467; PubMed=4721748;
MDDLINE=7327467; PubMed=4721748;
MAdreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
Riniker B., Rittel W., Sieber P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypoparathyroidism.";
J. Clin. Invest. 86:1084-1087(1990)
                                                                           PROTEIN SEQUENCE OF 75-100.
Keutmann H.T., Niall H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [12]
STRUCTURE BY NMR OF 32-65.
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Pubmed=10523031;
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RESULT 2 PTHY\_MACFA

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TISSUB-PCR rescued clones;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETABLEPCR RE.L.; Feingold B.A., Grouse L.H., Derge J.G.,

RIGURINE R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Altschul S.F., Jordach H., Moore T., Max S.I., Wang J., Haich F.,

By Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RIGHTON M., Soares M.B., Prefers G.J., Abramson R.D., Mullahy S.J.,

Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Romstein M.J., McKernan K.J., Malek J.A., Glubs R.D.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Romerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Romerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Romerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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VUCLECTIDE SEQUENCE.
MUCLECTIDE SEQUENCE.
MEDLINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;
Caecano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.1%; Score 125; DB 2; Length 115; 83.9%; Pred. No. 1.3e-08; Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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PARATHYROID; 1.
17861 MW; 849015736A6E5597 CRC64;
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Mammalia, Eutheria, Laurasiatheria, Perissodactyla,
NCBI_TaxID=9796;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, BC096143, AAH96143.1, -; mRNA.
EMBL, BC096144, AAH96144.1, -; mRNA.
EMBL, BC096145; AAH96145.1; -; mRNA.
EMBL, BC096142; AAH96142.1, -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
ProDom; PD010687; Pthyrhorm sub; 1.
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InterPro; IPR003625; Pthyrhorm_sub.
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Parathyroid hormone (Fragment).
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NIH MGC Project;
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Q9NIVO;
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SEQUENCE 115 AA;
                                                                                  NCBI_TaxID=9606;
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Malalavijtunond S., Takenaka O.;
"Nucleotide sequences of parathyroid gene in five species of macaque
of Thailand.";
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-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Cercopithecidae, Cercopithecidae, Macaca.
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By similarity.
Parathyroid hormone.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Parathyroid hormone, preproprotein.
                                                                                                                                                                                                                                                      16-CCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
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Pred. No. 1.3e-08;
      Pred. No. 1.3e-08;
1; Mismatches 4
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HSSP; P01270; 1ET1.
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InterPro; IPR001415; Parblyrhorm sub.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
Fram; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
SYART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHXROID; 1.
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Best Local Similarity 83.9%;
Matches 26; Conservative
    83.98;
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Q4VB48;
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Euteleostomi; Equidae; Equus.

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Gene 28:319-329(1984).
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BUBLINES 90056617, PubMed=388425;

Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,

Potts J.T. Jr., Rich A.;

Potts J.T. Jr., Rich A.;

Potts J.T. Jr., Rich A.;

Preproparathyroid hormone.";

Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985 (1979).
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NUCLEOTIDE SEQUENCE.
Weaver C.A., Gordon D.F., Kemper B.;
Wintroduction by molecular cloning of artifactual inverted sequences at the 5' terminus of the sense strand of bovine parathyroid hormone cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                 NoticeOlle Section A.R., Lyons L.A., O'Brien S.J., Laughlin T.F., Murray J.D., Bowling A.T.;

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF13433; AAF6237.1; -; Genomic_DNA.

EMBL, AF13423; AAF6237.1; -; Genomic_DNA.

GO, GO:000576; C:extracellular region; IEA.

GO, GO:000576; F:hormone activity; IEA.

InterPro; IPR001415; Parathyrd hrm.

InterPro; IPR003625; Phythrorm sub.

PANTHER; PTHR10541; Pthyrhorm sub.

ProDom; PD010667; Pthyrhorm sub; 1.

ProDom; PD010667; Pthyrhorm sub; 1.
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WICLEOTIDE SEQUENCE.

MEDLINE=83105564; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8; Meaver C.A., Gordon D.F., Kemper B.;

"Nucleotide sequence of bovine parathyroid hormone messenger RNA."; Moleotide Sequence of Servine Parathyroid hormone messenger NA."; Mol. Cell. Endocrinol. 28:411-424(1982).
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WUCLECTIDE SEQUENCE.

MEDLINE=64262463; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
Isolation and complete nucleotide sequence of the gene for bovine parathyroid hormone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecoza; Bovidae; Bovinae; Bos.
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Bowling A.T., Murray J.D.;
"A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1229-1249(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 AA; 9805 MW; 253184EA681A2022 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
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Pred. No. 3.2e-08;
2; Mismatches 4;
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Local Similarity 80.6%;
les 25; Conservative
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NUCLEOTIDE SEQUENCE.
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Matches
   RRARENTA BORROLL SELVINION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pp
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WEDLINE-7014666 pubMed-852780;
A Hanilton J.W., Nall H.D., Jacobs J.W., Keutmann H.T., Potte J.T. Jr.,
A Hanilton J.W., Nall H.D., Jacobs J.W., Keutmann H.T., Potte J.T. Jr.,
A Hanilton J.W., Nall H.D., Jacobs J.W., Keutmann H.T., Potte J.T. Jr.,
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                                                                       Gaps
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-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.

-!- SIBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
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MEDLINE=76018954; PubMed=1164500;
Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
"Porcine proparathyroid hormone. Identification, biosynthesis, and partial amino acid sequence.";
Biochemistry 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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74.4%; Score 119; DB 1; Length 115; 80.6%; Pred. No. 8e-08; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE #715-238: PubMed=3628009;
Schmelzer H.-J., Gross G., Widera G., Mayer H.;
Nuclectide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
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9FE8BCDE614BAC16 CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
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SIGNAL 1 25
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InterPro; IPR001625; Pthyrhorm sub.
PANTHER; PTHR10541; Pthyrhorm sub; 1.
Pfan; PPO1279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
SWART; SM00087; Pthyrhorm sub; 1.
PROSITE; PS00335; PARATHYROID; 1.
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PIR; B26806; PTPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 115 P.
115 AA; 12852 MW;
   Query Match
Best Local Similarity 80.6'
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig)
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SEQUENCE
                                                                                                                                                                                                                                                                                                    RESULT 6
PTHY PIG
ID PTHY PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=PTH
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                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Parathyroid;
MEDLINE=9356966; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;
Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W.,
Capen C.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequences of the cDNAs encoding canine parathyroid hormone-related protein and parathyroid hormone.";

Gene 160:241-243(1995).
-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
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Query Match 73.1%; Score 117; DB 1; Length 115; Best Local Similarity 77.4%; Pred. No. 1.5e-07; Matches 24; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U15662; AAA82584.1; -; mRNA.
PIR; JC4202; JC4202.
HSSP; P01268; IZWC.
Ensembl; ENSCAFG00000008177; Canis familiaris.
InterPro; IPR001415; Parathyrd, hrm.
InterPro; IPR001415; Parathyrd, hrm.
PANTHER; PTHR10541; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
PIRSF001832; PTH; 1.
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By similarity.
Parathyroid hormone.
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01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                 115 AA.
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                                                                                                                                 SUSEIQLMHNLGKHLSSLERVEWLRKKLQDV
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SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
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                                                                                                                                                                                                                                                                                 STANDARD;
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STANDARD;
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32
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115 AA;
  TISSUE=Parathyroid;
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CONFLICT
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PTHY_FELCA
     SOUTH THE FEET THE SOUTH T
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                                                                                                                                                Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Murbidae; Murinae; Rattus.
[1]
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Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
"Gene encoding parathyroid hormone. Nucleotide sequence of the rat
gene and deduced amino acid sequence of rat preproparathyroid
hormone."; Biol. Chem. 259:3320-3329(1984).
                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley;
MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
Nutley M.T., Parimi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger ribonucleic acid.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 68.8%; Score 110; DB 2; Length 10
1 Similarity 74.2%; Pred. No. 1.1e-06;
23; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00335; PARATHYROID; 1.
SEQUENCE 105 AA; 11684 MW; 18EE71B3F1CF5F70 CRC64;
Q80W22;
040.0203 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Napothalanic parathyroid hormone.
Name-PTH-(1-84);
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTHY RAT

AC D04089, D63473;
AC D04089, D63473;
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name-Pth;
SM Rattus norvegitus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology 136:5600-5607(1995).
EMBL, S80127, AAP32220.1; -; mRNA.
HSSP, P01270; 1ZWB.
GO: GO:0005576; C:extracellular region; IEA.
GO: GO:0005179; F:hormone actrvity; IEA.
INCEPPO: IPR001415; Parathyrd hrm.
INCEPPO: IPR003625; Pthyrhorm sub.
PANTHER; PTHRIO1541; Pthyrhorm sub.
PIRSF; PTRSF001832; PTH; 1.
PIODOM; PD101687; Pthyrhorm_sub; 1.
PINSF; SN00087; PTH; 1.
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NUCLEOTIDE SEQUENCE OF 10-115.
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uodin T.B., Toshiyuki S., Carninoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
N. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Russell J., Sherwood L.M.; "Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone mRNA and the deduced sequence of the hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL_2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AF066075; AAC99656.1; -; Genomic_DNA.
EMBL; BC099456; AAH99456.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                parathyroid hormone.
DA43FABBCB4E2FD9 CRC64;
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67.5%; Score 108; DB 2;
Best Local Similarity 71.0%; Pred. No. 2.3e-06;
Matches 22; Conservative 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Parathyroid hormone precursor (PTH).
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NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Thyroid;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
                                                                                                                                                                                                                               "Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
"Molecular cloning of feline preproparathyroid hormone.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Belongs to the parathyroid hormone family.
                          Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
By similarity.
Parathyroid hormone.
, 80CD557CC6AlA47E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
Pfan; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
ProDom; P0010687; Pthyrhorm_sub; 1.
SMART; SM00087; PTH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF309967; AAG30545.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 BY
31 BY
115 Pa
12921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2005 (TrEMBLrel, 31, La Parathyroid hormone precursor.
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Q9ZOL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
32 1
115 AA;
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                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                      Felinae, Felis.
NCBI_TaxID=9685;
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1D 022016 MOSE
1D 022016 MOST
1D 1 MAY-15
1D 1 01-MAY-15
1D 1 01-MAY-
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42.5%; Score 68; DB 2; Length 91;
46.7%; Pred. No. 0.38;
ive 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                   10647 MW; 75BBA25CEA64BF68 CRC64;
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0007595; P:lactation; IEA.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR003425; Pthyrhorm_sub.
InterPro; IPR003425; Pthyrhorm_sub.
PANTHER; PTHR1054; Pthyrhorm_sub; IPR037; Parathyroid; I.
ProDom; PD0110687; Pthyrhorm sub; I.
ProDom; PD0110687; Pthyrhorm sub; I.
ProDom; PD011055; PTH related; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 ISEVQLMHNVREHKQVGERQDWLQEKLKDV 60
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Best Local Similarity 46...
Best Local Similarity 46...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                             PTH;
                                                                                                                                                                                                                                                                                                                                                          91 AA;
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                                                                                                                                                                                                                                                                                                                             SMART; SM00087;
SEQUENCE 91 A
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                         MUCLECTIDE SEQUENCE.

MEDLINE=89284968; PubMed=3251402;

MEDLINE=89284968; PubMed=3251402;

MACHOELDE S. Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,

Minclectide sequence of cloned cDNAB encoding chicken

Treproparathyroid hormone.";

Treproparathyroid hormone.";

J. Bone Miner. Res. 3:689-698(1988).

- I-FUNCTION: PTH elevates calcium level by dissolving the salts in

Done and preventing their renal excretion.

- SIMILARITY: Belongs to the parathyroid hormone family.

- SIMILARITY: Belongs to the parathyroid hormone family.

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The Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its

cuse as long as its content is in no way modified and this statement is not
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Geneure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
Bastepe M., Rubin D.A., Juppner H.;
"Identification and characterization of two parathyroid hormone-like molecules in zebrafish.";
Endocrinology 145:1634-1639(2004).
EMBL; AX302221; AAQ73561.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL 1 25
PROPEP 26 31
PROPEP 26 119 Parathyroid hormone.
SEQUENCE 119 AA; 13943 MW; B309D8E772997F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M31604; AAA49093.1; -; mRNA.
EMBL; M46522 AAB02866.1; -; mRNA.
HSSP; D01270, 1FVY.
HSSP; D01270, 1FVY.
INCEMPL; ENGSALGO000005388; Gallus gallus.
INCEPPC; IPR001415; Parathyrd.hrm.
INCEPPC; IPR003426; PTL-redated.
INCEPPC; IPR003426; PTL-redated.
PROFINER; PTR15041; PCHYPHORM sub.
PRAM: PP01279; Parathyrorm sub; 1.
PIRSF; PIRSF001832; PTH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD013225; PTH_related; 1. ProDom; PD010687; Pthyrhorm_sub; 1. SRART; SM0087; PTH; 1. PROSITE; PS00335; PARATHYROID; 1. Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Parathyroid hormone type-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEW9J4 FUGRU PRELIMINARY;
QEW9J4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      removed
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Matches
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Ewropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!-SIMILARITY: Belongs to the parathyroid hormone family.
-!-CAUTION: 14 of the 15 residues are identical to an internal region of human parathyroid hormone. That seems quite an incredible
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial; Chitin-binding; Direct protein sequencing; Fungicide
25-0CT-2004 (Rel. 45, Created)
25-0CT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Chitin-binding protein HM30 (Fragment).
Hydrangea macrophylla (Bigleaf hydrangea)
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Sprmatophyta, Magnoliophyta, endicotyledons; core eudicotyledons; asterids; Cornales; Hydrangeaceae; Hydrangea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER 15 15 AA; 1875 MW; 7EE51EEC7D5B84DD CRC64;
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RY MUCLEGIDES SEQUENCE.

RY MEDLINE=20314478; PubMed=10854780; DOI=10.1016/S0378-1119(00)00167-0; RA MEDLINE=20314478; PubMed=10854780; DOI=10.1016/S0378-1119(00)00167-0; RA MEDLINE=20314478; PubMed=10854780; D.M., Canario A.V.M., Danks J., Elgar G., Clark M.S.; RI Genomic structure and expression of parathyroid hormone-related RT Genomic structure and expression of parathyroid hormone-related RT Genomic structure and expression of parathyroid hormone-related Genomic So:67-76(2000)

RY Genomic So:67-76(2000)

RY Genomic So:67-76(2000)

RY Genomic So:67-76(2000)

RY Good So:000579; Finamene activity; IEA.

DR GO; GO:0005795; P:hormone activity; IEA.

DR HORPERO; IPR001415; Parathyroid; I.

PRODOM; PPOLOM; PPOL129; PTH_related; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Fugur rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acathomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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45.2%; Pred. No. 1.7;
tive 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 34 Potential.
163 AA; 18698 MW; 3AC5F2C764732278 CRC64;
                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Parathyroid hormone-related protein precursor.
Name=PTHrP;
                                                                                            163 AA.
                                                                                            PRT;
                                                                                   Q918E9 FUGRU PRELIMINARY;
Q918E9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 45.2
nes 14, Conservative
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RESULT 15
(991819)
PUG
(991819)
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Search completed: November 21, 2005, 16:15:11 Job time : 148.5 secs

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Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence 1

Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 7, Sequence 1 Sequence 1 Sequence 1

Sequence 2, Al Sequence 1, Al Sequence 1, Al Sequence 13,

Sequence Sequence Sequence

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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GENERAL INFORMATION:
APPLICANT: Solick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Bioppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER E. Floppy disk
COMPUTER E. Floppy disk
COMPUTER F. Floppy disk
COMPUTER F. Floppy disk
COMPUTER F. Floppy disk
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
RAICH APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
RAICH APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: SWISS GENERAL ON NUMBER: 30,113
RESISTRATION NUMBER: 30,113
RESISTRATION NUMBER: 30,113
US-09-447-800-9
US-07-765-373-1
US-08-03-20-1
US-08-262-495C-1
US-08-2443-863-1
US-08-443-863-1
US-08-448-105-7
US-08-449-500-1
US-08-449-500-1
US-08-449-317A-1
US-08-449-447-1
US-08-444-328-1
US-08-444-328-1
US-08-414-326-2
                                                                                                                                                                                                                                                                                                                                                                  Sequence 46, Application US/08142551B Patent No. 5814603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPERENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEPAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: protein
      amino acid
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US-08-142-551B-46
    Appli
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32, Appl
2, Appli
1, Appli
6, Appli
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Sequence 17, Appl
Sequence 18, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                  November 21, 2005, 16:05:03; Search time 33 Seconds (without alignments) 77.665 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 162,
Sequence 163,
Sequence 52, A
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Sequence 32,
Sequence 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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US-09-623-548A-271
US-09-657-276-271
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-536-785A-6
                                                                                                                                                                                                                                                                   572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                              US-09-475-158A-3
160
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                          Post-processing:
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Result No.

us-09-475-158a-3.rai

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; FEATURE:

NAMEKEY: MOD_RES

: LOCATION: (1)

: OTHER INFORMATION: Desamino Ala
US-09-447-800-5
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                                           /note= "Where "Xaa" is selected
from the group consisting of Hol, Ho, a homoserine
amide, or the sequence of amino acids comprising
residues 35-84 of PTH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-OUL 6
US-09-447-800-6
US-09-447-800-6
Sequence 6, Application US/09447800
Sequence 6, Application US/09447800
Sequence 7, Application US/09447800
SEQUENCE 6, Application US/09447800
SEQUENCE 7 PARAMOTICAL SET OF SEQUENCE SEQU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORNERAL INFORMATION:
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKSU, HISABHI
APPLICANT: TAKSU, HISABHI
APPLICANT: GARDELLA, THOMAS J.
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMALOGS
FILE REFERENCE: 0609-4630001
CURRENT APPLICATION NUMBER: US/09/447,800
CURRENT APPLICATION NUMBER: US/09/447,800
CURRENT APPLICATION NUMBER: 0999-11-25
EARLIER FILING DATE: 1999-11-25
SOFTWARE: PACHOLIN VOS: 10
SOFTWARE: PACHOLIN Ver. 2.1
LENGTH: 34
TYPE: PRT
TYPE: PRT
CORGANISM: Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                           Length 35;
                                                                                                                                                                                                                                                                                                Query Match

80.6%; Score 129; DB 1; Length 35
Best Local Similarity 80.6%; Pred. No. 5.8e-10;
Matches 25; Conservative 3; Mismatches 3; Indels
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; Patent No. 6537965
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Desamino Ala
US-09-447-800-6
LOCATION: 35
; OTHER INFORMATION: /
; OTHER INFORMATION: 6
; OTHER INFORMATION: a
US-08-142-551B-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-447-800-5
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US-09-044-536A-12
i Sequence 12, Application US/09044536A
i Patent No. 6025467
i Patent No. 6025467
i APPLICANT: PUNCOMAN, Shizue
APPLICANT: HABASHITA, Junko
i APPLICANT: TAKETONI, Shigehisa
i TITLE OF INVENTION: RAATHYROID HORMONE DERIVATIVES AND THEIR USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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0
Query Match 80.0%; Score 128; DB 2; Length 34; Best Local Similarity 87.1%; Pred. No. 7.5e-10; Matches 27; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY:
COMPUTER:
C
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; JOHER INFORMATION: /product= "Xaa=Ala(2-Naph)"
(%-09-044-336A-12
                                                                                                                                                                                                                                                    1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                      1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: partial peptide LOCATION: 1..34
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Sequence 162, Application US/09843221A

Sequence 162, Application US/09843221A

Sequence 162, Application US/09843221A

Sequence 162, Application US/09843221A

GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL

APPLICANT: LIU, CHUNA-FA

APPLICANT: LIU, CHUNA-FA

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H

TITLE OF INVENTION: NOBER: US/09/843,221A

CURRENT APPLICATION NUMBER: US/09-26

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-26

PRIOR PRILING DATE: 2000-04-26

PRIOR PRILING DATE: 2001-02-06

PRIOR PRILING DATE: 2000-04-26

PRIOR PRILING DATE: 2000-04-26

PRIOR DATE: 2000-04-27

NUMBER: 60/200,053
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US-09-1-164
US-09-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Preferred embodiments - PTH
                                                                                              1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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APPLICANT: KOSTENUIK, PAUL
APPLICANT: KOSTENUIK, PAUL
APPLICANT: LIU, CHUAN-FA
APPLICANT: LACEY, DAVID LEB
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE TITLE OF INVENTION: RELATED PROTEIN
FILE REFREENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT PILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PALENTING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 18
LENGTH: 34
                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
APPLICANT: LIU, CULAN-FE
APPLICANT: LIU, CULAN-FE
TITLE OF INVENTION: MELATED PROTEIN
TITLE OF INVENTION: RELATED PROTEIN
FILE REFERENCE: A-658
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
PRIOR PILLING DATE: 2001-02-06
PRIOR FILLING DATE: 2000-06-28
PRIOR FILLING DATE: 2000-06-28
PRIOR FILLING DATE: 2000-06-28
PRIOR FILLING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SSCTURENT FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SSCTURENT FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SSCTURENT FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SSCTURENT FILING DATE: 2000-04-27
SSCUL NO 17
LENGTH: 34
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SVSEIQLMHDXGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: modified human PTH US-09-843-221A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: modified human PTH US-09-843-221A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-843-221A-18
Sequence 18, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
                                                                                                                                                                                Sequence 17, Application US/09843221A
Patent No. 6756480
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Best Local Similarity 83.9
Matches 26; Conservative
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Best Local Similarity 80.6%; Pred. No. 1e-09; Matches 25; Conservative 3; Mismatches
                                                                              1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                   1 SVSEIQLLHNLGGHLNSLERVEWLRKKLQDV 31
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Best Local Similarity 80.6%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 35 amino acids
amino acid
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      ; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34) ... (34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus US-09-843-221A-163
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LOCATION: 35
LOCATION: 35
COTHER INFORMATION: /note= "Where "Xaa" is selected
COTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
COTHER INFORMATION: amide, or the sequence of amino acids comprising
COTHER INFORMATION: residues 35-84 of PTH."
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-142-551B-52

) Sequence 52, Application US/08142551B

) Patent No. 5814603

) GENERAL INFORMATION:

APPLICANT: Oldenburg, Kevin R.

APPLICANT: Selick, Harold E.

TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND

TITLE OF INVENTION: ECOMPOINDS WITH PTH ACTIVITY AND

TITLE OF INVENTION: COMPOUNDS SEQUENCES: 132

CORRESPONDENCE ADDRESSE:

STREET: 699 Prince Street

COUNTRY: Alexandria

STREET: USGINGA
                                                                                                                                                               Query Match 79.4%; Score 127; DB 2; Length 34; Best Local Similarity 83.9%; Pred. No. 1e-09; Matches 26; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.4%; Score 127; DB 1; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: us

ZIP: 22313

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CLASSIFICATION UNMER: US/08/142,551B
FILING DATE: 12-CUT-1993
PRIOR APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1992
PRIOR APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
PRILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: SWIES: GETAIR : 00324-010
TELEPHONE: (415) 854-875
INFORMATION FOREXT NUMBER: 00324-010
TELEPHONE: (415) 854-875
INFORMATION POWER SEQ. ID NO: 52:
SEQUENCE CHARACTERISTICE:
LANGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
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FEATURE:
FRATURE:
NAME/KEY: Modified-site
NAME/KEY: Modified-site
NAME/KEY: Modified-site
NOTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
OTHER INFORMATION: amide, or the sequence of amino acids comprising
CHER INFORMATION: residues 35-84 of PTH."
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RESULT 10
US-08-142-551B-56
US-08-142-551B-6
US-08-142-551B
Patent No. 5914603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
ITILE OF INVERTION: COMPOUNDS WITH PTH ACTIVITY AND
STREET: 699 Prince Street
CITY: ALexandria
STATE: Virginia
STATE: Virginia
COUNTRY: US
STATE: Virginia
COUNTRY: US
SOFTWARE: Patentin Release #1.0, Version #1.25
COUNTRY: PRODUCES: US 08/08/45.DS
SOFTWARE: Patentin Release #1.0, Version #1.25
COUNTRY: US
SOFTWARE: Patentin Release #1.0, Version #1.25
COUNTRY: US
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Jaconton DATA: APPLICATION DATA: AP
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Pred. No. 1e-09;
3; Mismatches 3; Indels
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APPLICANT: BALDER, Jean-Rene
APPLICANT: BALDER, Paul
APPLICANT: Neugebauer, witold
APPLICANT: Neugebauer, witold
APPLICANT: Neugebauer, witold
APPLICANT: Whitfield, James
APPLICANT: Willick, Gordon E.
APPLICANT: Willick, Gordon E.
TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES
TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSBEE: NIXON & VANDERHYE, P.C.
STREET: 1100 New YORK AVenue, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 31;
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Pred. No. 1.7e-09;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,647C
FILING DATE: August 2, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMB: CTAMFORD, ARTHUR R.
REGISTRATION NUMBER: 25,327
112 Kent Street, Suite 770,
                                                                                                                                                                                                                                                                                                                                                                                            US/08/262,495C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/262,49:
PLING DATE:
CLASSIFICATION S30
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE:
FILING DATE:
FILENCENTION:
NAME: EADES, No. 556940ris M.
NAME: EADES, No. 556940ris M.
REGISTRATION NUMBER: 5,263
REFERENCE/DOCKET NUMBER: 3,203
REFERENCE/DOCKET NUMBER: 
                                    CITY: Octawa
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-691-647C-1
; Sequence 1, Application US/08691647C
; Patent No. 5955425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

Best Local Similarity 83.9%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                            Sequence 8, Application US/09044536A
Patent No. 6025467
GENERAL INFORMATION:
APPLICANT: FUKUDA:
APPLICANT: NAKAGAWA, Shizue
APPLICANT: TAKETOMI, Shigehisa
TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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Patent No. 5556940
GENERAL INFORMATION:
APPLICANT: WILLICK, Gordon E.
APPLICANT: WHITFIELD, James F.
APPLICANT: SUREWICZ, Witold
APPLICANT: SUREWICZ, Witold
APPLICANT: NEUGRNBAUER, Witold
TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/09/044,536A FILING DATE: 19-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/62,871
FILING DATE: 12-UN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.8%; Score 126; DB 2; L
Best Local Similarity 83.9%; Pred. No. 1.4e-09;
Matches 26; Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIKE, BRONSTEIN, ROBERTS & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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TITLE OF INVENTION: PARATHYROID HORMONI
TITLE OF INVENTION: FOR THE TREATMENT ON THE TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CONLIN, David G
REGISTRATION NUMBER: 27,026
REGISCOMMUNICATION NUMBER: 4650:
TELECOMMUNICATION INFORMATION:
TELEPAX: (617)523-3400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: partial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 130 wall-
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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US-09-044-536A-8
                                                                                               US-09-044-536A-8
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US-08-262-495C-3
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US-08-691-647C-6

Sequence 6, Application US/08691647C

Sequence 7 User 1 Morey 1 More  1 More 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.1%; Score 125; DB 1; Length 31 Best Local Similarity 83.9%; Pred. No. 1.7e-09. Indels Matches 26; Conservative 1; Mismatches 4; Indels
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REFERENCE/DOCKET NUMBER: 1339-5
TELECOMMUNICATION:
TELEPHONE: (703) 816-4005
TELEFAX: (703) 816-4100
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              INPORTATION OF SECULD NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 31 amino acide TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: cyclic
MOLECULE TYPE: protein
US-08-691-647C-6
                                                                                                                                                                                                                                                                                                                                                                            / MOLECULE TYPE: protein
US-08-691-647C-1
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Gaps
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APPLICANT: Jean-Rene, Barbier
APPLICANT: Reugebauer, Witcold
APPLICANT: Reugebauer, Witcold
APPLICANT: Reugebauer, Witcold
APPLICANT: Reugebauer, Witcold
APPLICANT: Whitfield, James
APPLICANT: Whillick, Gordon E.
TITLE OF INVENTION: PRATHYROID HORMONE ANALOGUES FOR THE
TITLE OF INVENTION: TREATHYROID HORMONE AND FRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: ALINGTON OF 6110892th Glebe Rd. 8th Floor
CITY: ALINGTON OF 6110892th Glebe Rd. 8th Floor
STREET: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY WISA
COUNTRY: BEATON DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/904,760B
FILING DATE: 01-AUG-1997
CLASSIFICATION NUMBER: 06/691,647
FILING DATE: 02-AUG-1996
ATTORING MATE: 03-AUG-1996
ATTORING
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                                                               Sequence 1, Application US/08904760B
Patent No. 6110892
GENERAL INFORMATION:
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RESULT 15
US-08-904-760B-1
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1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31

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162, App
163, App
21, Appl
22, Appl
27, Appl
165, App
27, Appl
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Sequence 5, Appli
                                                                   November 21, 2005, 16:15:23 ; Search time 110.5 Seconds (without alignments) 117.219 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                               Published Applications AA Main:*

(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-09-843-221A-18
US-09-843-221A-162
US-09-999-608-17
US-09-999-608-18
US-09-999-608-18
US-10-899-608-162
US-09-999-608-162
US-10-839-037-163
US-10-839-037-163
US-10-839-037-163
US-10-839-037-163
US-10-839-037-163
US-10-839-037-163
US-10-839-037-163
US-10-839-037-163
US-10-893-038-22
US-09-843-221A-155
US-09-843-221A-155
US-09-999-608-165
                                                                                                                                           1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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US-10-839-037-165
                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                   1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                protein search, using sw model
                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                                                                  US-09-475-158A-3
160
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Match Length DB
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Perfect score:
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                                                OM protein -
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Maximum DB
                                                                                                                                            Sequence:
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Sequence 1, Appli
Sequence 1, Appli
Sequence 21, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 175, Appli
Sequence 193, Appli
                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10361928

Publication No. US20030144209A1

GENERAL INCOMATION:
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKASU, HISASHI
APPLICANT: GRABELLA, THOMAS J.
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMALOGS
FILE REPERENCE: 6069-4630002
CURRENT FILING DATE: 2003-02-11
PRIOR PLICATION NUMBER: 09/447,800
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SSOFTWARE: Patentin Ver. 2.1
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Publication No. US20030144209A1
GENERAL INFORMATION:
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKASU, HISASHI
APPLICANT: GARDELIA, THOMAS J.
TITLE OF INVENTION: AMNO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: ANALOGS
FILE REFERENCE: 0609-4630002
CURRENT APPLICATION NUMBER: US/10/361,928
               Sequence
Sequence
Sequence
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Pred. No. 2e-09;
0; Mismatches 4;
US-10-892-025-2
US-11-040-557-20
US-10-892-025-3
US-11-040-557-1
US-01-040-557-21
US-09-169-786-3
US-09-858-880-5
US-09-858-0478-6
US-09-843-221A-161
US-09-998-048-6
US-09-999-608-174
US-09-999-608-174
US-09-999-608-175
US-09-999-608-175
US-09-999-608-175
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US-09-999-608-175
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                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 80.0%; Scc
1 Similarity 87.1%; Pre
27; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Desamino Ala US-10-361-928-6
    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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    LENGTH: 33
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GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: LIU, CHURAN-FA

APPLICANT: LIU, CHURAN-FA

APPLICANT: LIU, CHURAN-FA

APPLICANT: LIU, CHURAN-FA

APPLICANT: LIU, CHURAN-FO

TITLE OF INVERTION: RELATED PROTEIN

FILE REFERENCE: A-665B

CURRENT PLING DATE: 2001-04-26

CURRENT APPLICATION NUMBER: 60/266,673

PRIOR PLING DATE: 2001-06-26

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2000-06-3

PRIOR PLING DATE: 2000-06-3

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PREDENTING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 162

LENGTH: 34

THORY PLING DATE: DATE

THORY PLING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 162

THE PRIOR PLING DATE: 2000-04-27

THORY PLING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 162
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NAME/KEY: misc feature
1. CATION: (34) - (34)
2. OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162
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79.4%; Score 127; DB 3;
Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4.
TITLE OF INVENTION: RELATED PROTEIN
FILE REFERENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/266,673
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-27
NUMBER: OF SEQ ID NOS: 170
SEQ ID NO 18
LENGTH: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 162, Application US/09843221A Publication No. US20030039654A1 GENERAL INFORMATION:
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US-09-843-221A-163
; Sequence 163, Application US/09843221A
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 26; Conserv
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US-09-643-221A-17

Sequence 17. Application US/09843221A

Publication No. US2030039654A1

Sublication No. US2030039654A1

Sublication No. US2030039654A1

APPLICANT: KOSTBUUIK, PAUL

APPLICANT: LIU, CHUAN-FA

APPLICANT: LIU, CHUAN-FA

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORROR APPLICATION NUMBER: US/09/843,221A

CURRENT APPLICATION NUMBER: US/09/843,221A

CURRENT APPLICATION NUMBER: 60/266,673

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SOFTWARE: Patentin version 3:1

SEQ ID NO 17
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Sequence 18, Application US/09843221A
Sequence 18, Application US/09843221A
PUBLICATION OF US20030039654A1
SERREAL INFORMATION:
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
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               CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: 09/47,800
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/110,152
PRIOR APPLICATION NUMBER: 60/110,152
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: modified human PTH US-09-843-221A-17
                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1) ; OTHER INFORMATION: Desamino Ala US-10-361-928-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES
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Best Local S:
Matches 27
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APPLICANT: KOSTEMUIK, PAUL
APPLICANT: GEGG COLIN V.
APPLICANT: KINSTLER, OLAF BORIS
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
TITLE OF INVENTION: LORDANE: 2002-03-11
TITLE REFERENCE: A-665C
CURRENT APPLICATION NUMBER: US 60/999,608
FRICH APPLICATION NUMBER: US 60/266,673
PRIOR APPLICATION NUMBER: US 60/214,860
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-27
SOGTWARE: PAVENTIN VAFFAIN 3.2
SOGTWARE: PAVENTIN VAFFAIN 3.2
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APPLICANT: GEGG, COLIN V.
APPLICANT: GEGG, COLIN V.
APPLICANT: GEGG, COLIN V.
APPLICANT: GEGG, COLIN V.
APPLICANT: GEGG, COLIN V.
APPLICANT: GEGG, COLIN V.
APPLICANT: GEGG, COLIN V.
APPLICANT: GEGG, COLIN V.
APPLICANT: HORSILER, OLAF BORIS
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
CURRENT APPLICATION NUMBER: US 60/999, 608
PRIOR FILING DATE: 2001-02-03-1
PRIOR PELING DATE: 2001-02-06
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-27
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Pred. No. 2.8e-09;
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                                                                                  1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31
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                          1 AVSEIQLMHGGGGGLNSMERVEWLRKKLODV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: modified human PTH
US-09-999-608-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-999-608-162

i, Sequence 162, Application US/09999608

i, Publication No. US20050124537A1

i, GENERAL INFORMATION:
                                                                                                                                                                                                                                     ; Sequence 18, Application US/0999608; Publication No. US20050124537A1; GENERAL INFORMATION:
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Best Local Similarity 83.9%;
Matches 26; Conservative 1
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SEQ ID NO 162
LENGTH: 34
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                                                                                                                                                                                                              US-09-999-608-18
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                                                                    g
                                                                              APPLICANT: LIU, CHUAN-FA

APPLICANT: LIU, CHUAN-FA

APPLICANT: LACEY, DAVID LEE

APPLICANT: LACEY, DAVID LEE

TITLE OF INVENTION: MODILALPORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H

TITLE OF INVENTION: MODILALDED RECTEIN

FILE REFRERENCE: A-665B

CURRENT APPLICATION NUMBER: US/09/843,221A

CURRENT FILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: 60/24,860

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PARENTE ABLEICATION NUMBER: 61/200,053

RIOR PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SSOFTWARE: PARENTE ABLEICATION NUMBER: 61/200,053

FRIOR FILING DATE: 3000-04-27

SSOFTWARE: PARENTE ABLEICATION NUMBER: 61/200,053

FRIOR FILING DATE: 3000-04-27

SSOFTWARE: PARENTE ABLEICATION NUMBER: 61/200,053

FRIOR PLING DATE: 3000-04-27

SSOFTWARE: PARENTE ABLEICATION NUMBER: 61/200,053

FRIOR PLING DATE: 2000-04-27

SSOFTWARE: PARENTE ABLEICATION NUMBER: 61/200,053
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| Sequence 17, Application US/0999608
| Publication No. US20050124537A1
| GENERAL INFORMATION:
| APPLICANT: GEGG, COLIN V.
| APPLICANT: GEGG, COLIN V.
| APPLICANT: GEGG, COLIN V.
| APPLICANT: MARK ANTHONY
| APPLICANT: MINSTLER, OLAF BORIS
| TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
| TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
| TITLE OF INVENTION: MODULATORS OF RECEPTORS
| TITLE OF INVENTION: MODULATORS OF RECEPTORS
| TITLE OF INVENTION: MODULATORS OF RECEPTORS
| FILE REFERENCE: A-665C
| CURRENT FILING DATE: 2002-03-11
| PRIOR PILICATION NUMBER: US 60/266,673
| PRIOR FILING DATE: 2001-02-06
| PRIOR PILING DATE: 2000-06-28
| PRIOR PILING DATE: 2000-04-27
| NUMBER OF SEQ ID NOS: 193
| SOFTWARE: PATENTIN VETRION 3.2
| SEQ ID NO 17
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// LOCATION: (34)...(34)...

OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-09-843-221A-163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.4%; Score 127; DB 3; Best Local Similarity 83.9%; Pred. No. 2.8e-09; Matches 26; Conservative 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Preferred embodiments - PTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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ORGANISM: Artificial Sequence
Publication No. US20030039654A1
GENERAL INFORMATION:
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Matches 26; Conservative
                                                              APPLICANT: KOSTENUIK, PAUL
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RESULT 12

US-10-819-037-18

US-10-819-037-18

Sequence 18, Application US/10839037

Publication No. US20040214996A1

GENERAL INVENTATION: PAUL

APPLICANT: LIU, CHUAN-FA

APPLICANT: NOWBER: US/10/839,037

TITLE OF INVENTION: RELATED PROTEIN

FILE REFERENCE: A-658

CURRENT APPLICATION NUMBER: US/09/843,221A

PRIOR PELLING DATE: 2001-02-06

PRIOR PELLOR DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/214,860

PRIOR APPLICATION NUMBER: 60/214,860

PRIOR PELLOR DATE: 2000-04-27

PRIOR PELLING DATE: 2000-04-27

PRIOR PELLING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PATCH LIN VETSION 3.1

SEQ ID NOS: 170

SEQ ID NOS:
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Best Local Similarity 83.9%; Pred. No. 2.8e-09;
Matches 26; Conservative 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVSEIQL/MHNKGKHL/NSMERVEWLRKKLQDV 31
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FILE OF INVENTION: RELATED PROTEIN
FILE REFRENCE: A-665B
CURRENT APPLICATION NUMBER: US/10/839,037
CURRENT FILING DATE: 2004-05-04
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-06-66,673
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 17
LENGTH: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: modified human PTH US-10-839-037-17
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-10-839-037-162
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US-09-999-608-163

Sequence 163, Application US/0999608

Publication No. US20050124537A1

GENERAL INFORMATION:
APPLICANT: GEGG, COLIN V.
APPLICANT: ARNSTER, OLAF BORIS
TITLE OF INVENTION: MOUNBER, US 08 RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
TITLE OF INVENTION: MOUNBER: US 09/943,221
FILE REFERENCE: A-665C
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/266,673
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 133
SEQ ID NO 163
LENGTH: 34
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; Sequence 17, Application US/10839037
; Sequence 17, Application US/20040214996A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in LOCATION: (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ... (14) ...
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NAME/KEY: misc feature
LOCATION: (34) - (34)
OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-999-608-162
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                                                                                                                                                                                             OTHER INFORMATION: Preferred embodiments - PTH
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                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 21, Application US/10892025

Publication No. US20050065071A1

GENERAL INFORMATION:

APPLICANT: Whitfield, James F

TITLE OF INVENTION: CYCLIC ANALOGS OF HUMAN PARATHYROID

TITLE OF INVENTION: HORMONE FOR THE TREATHENT OF CONDITIONS CHARACTERIZED BY

TITLE OF INVENTION: HORMONE FOR THE TREATHENT OF CONDITIONS CHARACTERIZED BY

TITLE OF INVENTION: HORMONE FOR THE TREATHENT OF CONDITIONS CHARACTERIZED BY

TITLE OF INVENTION: HYPERENCLIFERATIVE SKIN CELLS

FILE REFERENCE: 3583.1000-001

CURRENT APPLICATION NUMBER: US/10/892,025

CURRENT PILING DATE: 2003-07-15

NUMBER OF SEQ ID NOS: 42

SEQ ID NO 21

LENGTH: 31
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-10-839-037-163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT LOCATION: 12 LOCATION: 13 Selected from the group consisting of Lys, Orn, OTHER INFORMATION: 18 Selected from the group consisting of Lys, Orn, OTHER INFORMATION: Glu, Asp, Cys, and homocysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Y; where Y is X, His-X, His-Asn-X, or CTHER INFORMATION: His-Asn-Phe-X; X is OR or NHR; and R is hydrogen OTHER INFORMATION: or a linear or branched chain alkyl, acyl or aryl US-10-892-025-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: NHR; where R is hydrogen or a linear or branched OTHER INFORMATION: chain alkyl, acyl or aryl group PEATURE:
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                                                                                                            Score 127; DB 4;
Pred. No. 2.8e-09;
1; Mismatches 4
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                                                                                                               Query Match
Best Local Similarity 83.9%;
Matches 26; Conservative
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ORGANISM: Homo sapien
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Sequence 163, Application US/10839037

Publication No. US20040214996A1

GENERAL INFORMATION:
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MOULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: RELATED PROTEIN
FILE REFERENCE: A-665B
CURRENT FILING DATE: 2004-05-04

PRIOR APPLICATION NUMBER: US/09/843,221A
PRIOR APLICATION NUMBER: 60/214,860
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2000-04-27

PRIOR PILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/210,053
PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 163

LENGTH: 34

LENGTH: 34
                                                                                    GENERAL INCREMININ, PAUL
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
TITLE OF INVENTION: RELATED PROTEIN
FILLE REFERENCE: A-6658
CURRENT APPLICATION NUMBER: US/10/839,037
CURRENT PELING DATE: 2004-05-04
PRIOR PPLICATION NUMBER: US/99/843,221A
PRIOR APPLICATION NUMBER: 60/266,673
PRIOR APPLICATION NUMBER: 60/266,673
PRIOR FILING DATE: 2000-02-06
PRIOR FILING DATE: 2000-02-06
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 170
SSOFTWARE: PARCHIN VERSION 3.1
LENGTH: 34
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; LOCATION: (34)...(34)...

; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-10-839-037-162
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Pred. No. 2.8e-09;
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                  Sequence 162, Application US/10839037
Publication No. US20040214996A1
GENERAL INFORMATION:
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Best Local Similarity 83.9%;
Matches 26; Conservative
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November 21, 2005, 16:16:29 ; Search time 4 Seconds (without alignments)
8.756 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	1	Appl	Appl	Appl	, App	Appl	, App	App	App	App	3, App	ppli	Appli	, pp]i	App	Appl										
	E	29,	28,		256,	21,		726,	464,	720,	723,	4, 4	7,7	3, 2	340,	20,	22,	24,	26,	28,	30,	32,	34,	36,	38,	10,
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence
	ID	US-10-512-184-29	US-11-082-389-28	US-10-957-569-64	US-11-074-176-256	US-11-004-057-21	US-10-939-890-474	US-10-939-890-726	US-10-939-890-464	US-10-939-890-720	US-10-939-890-723	US-11-004-057-4	US-11-077-978-7	US-11-084-408-3	US-10-131-826A-340	US-11-065-943-20	US-11-065-943-22	US-11-065-943-24	US-11-065-943-26	US-11-065-943-28	US-11-065-943-30	US-11-065-943-32	US-11-065-943-34	US-11-065-943-36	US-11-065-943-38	US-10-967-648A-10
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Sequence 9, Appli	Sequence 78, Appl	Sequence 94, Appl	Seguence 99, Appl	Sequence 4, Appli	Sequence 10, Appl	Sequence 32, Appl	Sequence 6, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 24, Appl	Sequence 16, Appl	Sequence 8, Appli	Sequence 12, Appl	Sequence 33, Appl	Sequence 68, Appl	Seguence 45, Appl	Sequence 46, Appl	Sequence 37, Appl	Sequence 8, Appli
US-10-789-273-9	US-11-074-176-78	US-10-131-826A-94	US-10-467-962B-99	US-10-789-273-4	US-10-789-273-10	US-11-144-248-32	US-10-997-201A-6	US-11-077-978-2	US-11-077-978-3	US-11-144-248-24	US-11-144-248-16	US-10-789-273-8	US-10-789-273-12	US-10-721-763-33	US-10-510-386-68	US-11-144-248-45	US-11-144-248-46	US-10-972-587-37	US-10-499-715-8
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26	27	28	53	30 3	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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17.10-15.12-18.2
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RESULT 5

US-11-004-057-21

US-11-004-057-21

SQUENCE 21, Application US/11004057

Publication No. US20050244846A1

GENERAL INFORMATION:

APPLICANT: Johnson, Gary L.

TITLE OF INVENTION: MEKKI PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING TITLE OF INVENTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION: APPLICANTION NUMBER: US/11/004,057

CURRENT APPLICATION NUMBER: US/11/004/03.75

PRICR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 21

SOFUTON NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                     APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Alternann, Eric
APPLICANT: Alternann, Eric
APPLICANT: Andrea Azcarate
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICANTION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICANTION NUMBER: 60/551,161
PRIOR PELICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2006-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.5%; Score 44; DB 7; Length 1213; 25.6%; Pred. No. 26; tive 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GLNSMERVEWLRKK 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Satto, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dramsfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Pan, Hong
APPLICANT: Pan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SEIQLMHGGGG------
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; ORGANISM: Rattus norvegicus
US-11-004-057-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 GGGGGLN-----
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Best Local Similarity 25.6
Matches 11; Conservative
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Publication No. US20050246785A1

Publication No. US20050246785A1

Publication No. US20050246785A1

APPLICAMT: COOK, Jahinong et al.

TITLE OF INVENTION: THEREOF

FILE REPRENDE: 2750-157791833

CURRENT APPLICATION NUMBER: US/10/957,569

CURRENT PILING DATE: 2004-09-30

PRIOR PILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin version 3.3

SEQ ID NO 64
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CURRENT FILING DATE: 2005-03-16

PRIOR PAPLICATION NUMBER: US 09/603024

PRIOR PELLING DATE: 2000-06-23

PRIOR PELLING DATE: 1999-06-25

PRIOR PELLING DATE: 1999-06-25

PRIOR PELLING DATE: 1999-06-26

PRIOR PELLING DATE: 1999-07-09

PRIOR PELLING DATE: 1999-07-09

PRIOR PELLING DATE: 1999-07-01

PRIOR PELLING DATE: 1999-07-08

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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 256, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
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RESULT 3 US-10-957-569-64

ò g ORGANISM: Arabidopsis thaliana US-10-957-569-64

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US-11-074-176-256

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LOCATION: (28)..(28)
OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SOUN, BOLE
APPLICANT: SOUN, BOLE
APPLICANT: Won Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
TILE REPERENCE: D0647700140500
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-15
PRIOR FILING DATE: 2003-03-15
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PRIOR FILING DATE: 2003-01-15
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Pred. No. 0.86;
2; Mismatches
PRIOR FILING DATE: 2003-03
PRIOR FILING DATE: 2003-03
PRIOR PILING DATE: 2003-03
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 726
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 464, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
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Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palanlappa
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
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Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::||||||
20 ILHGGGGG 27
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APPLICANT:
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                                                                                                                                                                                                        APPLICANT: SWEIGOL, KOIL E.

APPLICANT: SWEIGOL, KOIL E.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR PILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 0/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/40,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFREEDE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US/661,156
                           Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Sequence 726, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
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Ramalingam, Kondareddiar
Shrivastava, Ajay
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe APPLICANT: Fan, Hong APPLICANT: Fan, Hong APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nunn, Adrian D.
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  Marinelli, Edmund R.
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Swenson, Rolf E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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Best Local Similarity
Matches 6; Conserval
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20 ILHGGGGG 27
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Length 28; 0; Indels ۲;

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                                                             Query Match 25.0%; Score 40; DB 1; Length 28; Best Local Similarity 57.1%; Pred. No. 1.6; Matches 8; Conservative 3; Mismatches 1; Indels
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NAMEXKEY: MOD RES
LOCATION: (28)..(28)
COTHER INVORMATION: Lys residue modifed with a SATA linker
US-10-939-890-723
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APPLICANT: Song, Bo
APPLICANT: Weenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
ITITE OF INVEXTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPREMENCE: D0617.700140S00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-113
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-0-303
PRIOR PILING DATE: 2003-0-303
PRIOR FILING DATE: 2003-0-304
PRIOR FILING DATE: 2003-0-30-15
PRIOR FILING DATE: 2003-0-30-15
PRIOR FILING DATE: 2003-0-30-15
PRIOR FILING DATE: 2003-0-30-15
PRIOR FILING DATE: 2002-0-30-15
PRIOR PRIOR FILING DATE: 2002-0-30-15
PRIOR FILING DATE: 2002-0-30-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sarto, Aaron K.
APPLICANT: Sarto, Aaron K.
APPLICANT: Sarton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Fan, Hong APPLICANT: Fan, Hong APPLICANT: Fan, Hong APPLICANT: Marrinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinapan, Palaniappa APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna APPLICANT: Pillai, Radhakrishna APPLICANT: Pillai, Radhakrishna APPLICANT: Pillai, Radhakrishna APPLICANT: Pillai, Radhakrishna APPLICANT: Pillai, Radhakrishna APPLICANT: Pillai, Radhakrishna APPLICANT: Ramalingam, Kondareddiar APPLICANT: Sanalingam, Anay
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OTHER INFORMATION: Synthetic peptide
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US-10-939-890-723
; Sequence 723, Application US/10939890
; Sequence 723, No. US20050250700A1
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LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
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ORGANISM: Artificial sequence
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US-10-939-890-720
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OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (28)..(28)
OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
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25.0%; Score 40; DB 1; Length 28;
Best Local Similarity 57.1%; Pred. No. 1.6;
Matches 8; Conservative 3; Mismatches 1; Indels
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APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
TITLE OF INVENTION: KDR AND VEGFKOR BINDING PEPTIDES
FILE REFERENCE: DO617.700140500
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR PELLOATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/82,082
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: DC7/US03/06731
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FASESEQ for Windows Version 4.0
LENGTH: 2007
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 464
LENGTH: 28
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Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Manjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylla
Ramalingam, Kondareddiar
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Publication No. US20050250700A1
GENERAL INFORMATION:
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APPLICANT: Sexton, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Busset, Philippe
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ORGANISM: Artificial sequence
                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-10-939-890-720
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APPLICANT:
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APPLICANT: Spolski, Rosanne
APPLICANT: Spolski, Rosanne
APPLICANT: Kelly, John
APPLICANT: Kelly, John
APPLICANT: Kene-Myers, Andrea M.
TITLE OF INVENTION: METHODS FOR USE OF TSLP AND AGONISTS AND ANTAGONISTS THEREOF
FILE REFERENCE: 4239-67781-02
CURRENT PAPLICATION NUMBER: US/11/084,408
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2004-03-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Version 3.3
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/131,026A
CURRENT PILING DATE: 200-40-24
PRIOR PAPLICATION NUMBER: 60/05911
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
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7
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Pred. No. 34;
4; Mismatches 10; Indels
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                                                                                                Al-Shami, Amin
Spolski, Rosanne
Kelly, John
Keane-Myers, Andrea M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.4%;
38.5%;
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                                                  Lenord, Warren J.
Pandey, Akhilesh
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Goddard, Audrey
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Watanabe, Colin K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Rattus norvegicus US-11-084-408-3
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Gurney, Austin L.
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 38.5
Matches 10; Conservative
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                              HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-10-131-826A-340
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                                                                                                     APPLICANT:
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                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Johnson, Gary L.

TITLE OF INVENTION: REKEN PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING
TITLE OF INVENTION: APOPTOSIS
FILE REFERENCE: CPI-042CPPC
CURRENT APPLICATION NUMBER: US/11/004,057
CURRENT PILING DATE: 2004-12-02
PRIOR APPLICATION NUMBER: US/9/403,075
PRIOR FILING DATE: 2000-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/11077978

Sequence 7, Application US/11077978

Publication No. US20050244333A1

GENERAL INFORMATION:

APPLICANT: Sharaki, Paul J.

APPLICANT: Sharaki, Paul J.

APPLICANT: RaubiteChek, Andrew A.

APPLICANT: RaubiteChek, Andrew A.

TITLE OF INVERTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof

FILE REFERENCE: 54435.8012.US01

CURRENT APPLICATION UMMER: US/11/077,978

CURRENT FILING DATE: 2005-03-11

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.2
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Publication No. US20050249712A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 7; Length 120;
Pred. No. 10;
6; Mismatches 7; Indels
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Pred. No. 1.1e+02;
6; Mismatches 6;
                                                                                                                              Sequence 4, Application US/11004057
Publication No. US20050244846A1
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       14 ADLQLSHFAGGGGG 27
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1493
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Best Local Similarity 25.6
Matches 10; Conservative
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Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT CORGANISM: Mus musculus US-11-004-057-4
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US-11-065-943-20

US-11-065-943-20

Sequence 20, Application US/11065943

Publication No. US20060250131A1

GENERAL INFORMATION:
APPLICANT: USCHIECUBRE,
APPLICANT: VICHIER-UUC

APPLICANT: VICHIER-UUC

TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

TITLE OF INVENTION: WARLANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITES,
TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
FILE REPRENCE: 2664-261830XCIP

CURRENT APPLICATION NUMBER: US/11/065,943

CURRENT APPLICATION NUMBER: US/11/065,943

FRIDA APPLICATION NUMBER: US/11/065,943

FRIDA APPLICATION NUMBER: US/11/065,943

SOFTWARE: PALENTING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SOFTWARE: PALENTIN VERSION 3:3

SEQ ID NO 20

LENGTH: 562

THE THE TENT NUMBER: US/11/065,943

FRIDE APPE: PALENTING DATE: 2004-02-27

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SOFTWARE: PALENTING DATE: 2004-02-27

FRIDE APPE: PALENTING DATE: 2004-02-27

FRIDE APPE: PALENTING DATE: 2004-02-27

FRIDE APPRICATION NUMBER: US/11/065,943

FRIDE APPRICATION NUMBER: US/11/0787,219

FRIDE APPRICATION THE TENT NUMBER: US/11/0787,219

FRIDE APPRICATION THE TENT NUMBER: US/11/065,943

FRIDE APPRICATION THE TENT NUMBER: US/11/0787,219

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PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR APPLICATION NUMBER: 60/059588
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
LENGTH: 386
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Pred. No. 54;
2; Mismatches 6; Indels
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Best Local Similarity 42.9%;
Matches 6; Conservative 2
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                                                     November 21, 2005, 15:52:37 ; Search time 141.5 Seconds (without alignments) 96.260 Million cell updates/sec
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Abj10713
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                            2443163 segs, 439378781 residues
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                                    using sw model
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AAY96975
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1990s:*
2: geneseqp1990s:*
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6: geneseqp2003as:*
7: geneseqp2003as:*
8: geneseqp2003as:*
9: geneseqp2004s:*
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Maximum Match 100%
Listing first 45 su
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Perfect score:
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Aar21178 Human par Aar21236 Human par Aar21235 Human par Aar21259 Human par Aar2229 Human par Aar74457 Purachtyro Aar7446 Parachtyro Aar74470 Parachtyro Aar74470 Parachtyro Aar74470 Parachtyro Aar21231 Human par Aar21231 Human par Aar21232 Human par Aar21231 Human par Aar21312 Bovine pa Aar21376 Human par Aar2176 Human par Aar496915 Human mar Aar49691 Sequence Aaw47943 Human par Aav17941 Human par Aav17941 Human par Aav17941 Human par Aav17941 Human par Aav17941 Human par			igate peptide PG9.	mass; bone reformation; sis.		signaling_domain	in a section						Jueppner H;		signaling functional domain on of parathyroid hormone for id by decreases in bone mass.
84 2 AAR21178 84 2 AAR21234 84 2 AAR21235 84 2 AAR21235 35 2 AAR74457 35 2 AAR74457 35 2 AAR74457 35 2 AAR74457 35 2 AAR74457 36 2 AAR72123 84 2 AAR21231 84 2 AAR21231 84 2 AAR21231 84 2 AAR78915 34 2 AAR49697 34 2 AAR49697 34 2 AAR49697 34 2 AAR49697 34 2 AAR49697 34 2 AAR49697 34 2 AAR49697	ALIGNMENTS d; peptide; 31 AA.	(first entry)	one functional domain conjugate	parathyroid hormone; conjugate; bone ma rption; remodeling; tether1; osteoporosi		e inal_	linke in n	/laber= residues 15-31"		99WO-US031108.	98US-0114577P.	л т J. SRG н м. Т. ? н.	Kronenberg HM, Potts JT, Ju	1/39. L	New compound comprising an amino terminal sign. linked to a carboxy-terminal binding portion o treating mammalian conditions characterized by
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	standard;		id hormone	hyroic 1, remc	ens.			-A2.	. 00			GARDELLA T KRONENBERG POTTS J T. JUEPPNER H	TJ, K	00-452384/3 AAA51731.	und cor a carl mammal:
00000000000000000000000000000000000000	96974	AAY96974; 31-OCT-2000	arathyroid	PTH; parath resorption;	Homo sapie Synthetic.	Key Peptide	Peptide Peptide	WO200039278	06-JUL-2000	0-DEC-1999	1-DEC-1998	(GARD/) G. (KRON/) KI (POTT/) PK (JUEP/) JI	Gardella '	WPI; 2000 N-PSDB; A	lew compor inked to reating 1
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Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. Si as an amino terminal signaling functional domain of parathyroid hormone (PTH); Lis a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-134) or a PTH-reated protein (PTH-rP) (1.134); R. I is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor agreemen; and R is (a portion of) PTH-1 receptor adjunction are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling treating diseases and disporder associated with decreased tether! activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inchalacion unlike the large native PTH or PTH or PTH which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis.
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Local Similarity 100.0%; Pred. No. 8.4e-13;
es 31; Conservative 0; Mismatches 0; Indels
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/label= PTH N-terminal_signaling_domain
/note= "resīdues 1-9"
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/note= "residues 15-31"
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                                    Claim 7; Page 93; 119pp; English
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/label= linker
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/label= PTH_C-to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US031108
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(KRON/) KRONENBERG H M.
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N-PSDB; AAA51729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200039278-A2
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Matches
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Gaps

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Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R are mind the parathyroid hormone (PTH); Lisa linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a Cterminal binding portion of PTH(-1,34) or a PTH-related protein (PTH-rP) (1-34), R. lis the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor show compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases in a mammalian cell having PTH-1 receptors, or screening for a popular in a mammalian cell having PTH-1 receptors, or screening for a peptide on non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHTP which avoids the need for regular injections to treat osteoporosis
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New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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                                                                                                                                                                                                                                                                                                                                                               Length 31;
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    .9
/label= PTH N-terminal_signaling_domain
/note= "residues 1-9"

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/label= PTH C-terminal_binding_portion
/note= "residues 17-31"
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Local Similarity 87.1%; Pred. No. 1.7e-08;
les 27; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVSEIQLMHGGGGGLNSMERVEWLRKKLQDV 31
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                                                                Claim 7; Page 92-93; 119pp; English
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/label= linker
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(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
(JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                   Sequence 31 AA;
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Synthetic.
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RESULT 5
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                                                                                                                                                                                            Compounds of the structure or formula S-(L) n-B, R.1-S-(L) n-R or S-(L) n-R, are new, S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH:P which avoids the need for regular injections to treat osteoporosis
                                                                  domain
rmone for
                                                               New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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Pred. No. 3.9e-07;
); Mismatches 0;
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|AVSEIQLMHGGGGGGG----SMERVEWLRKKLQDV
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                                                                                                                                                           Claim 7; Page 93; 119pp; English.
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77.18;
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N-PSDB; ADG93252.
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                       N-PSDB; AAA51730
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                   high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of an amino acid sequence encoded by an expression cassette of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified parathyroid hormone analogues - useful in treating cancer, osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
This invention relates to a novel expression cassette and methods for
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Pred. No. 4.1e-05;
0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human parathyroid hormone analogue, [Ala1Gly6]hPTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 VGGGGGPRSVSEIQLMHNLGKHLNSMERVEWLRKKLODV
                                                                                                                                                                                                                                                                                                                                                                                                                                 --GGGLNSMERVEWLRKKLQDV
                                                                                                                                                                                                                                                                                                                  Score 104; DB 8;
Pred. No. 3.3e-05;
1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR21190 standard; protein; 84 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 63.6%;
1 Similarity 77.4%;
24; Conservative C
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                                                                                                                                                                                                                                                                                                                        64.2%;
59.0%;
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(first entry)
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Best Local Similarity 59.0
Matches 23; Conservative
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                                                                                                                                                                                                                                                                        Sequence 89 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
17-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-1992
                                                                                                                                                                                                                   invention.
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growth hormone releasing factor; GRF; hydrolytic polypeptide cleavage; palladium promoter; formic acid; inclusion body; glucagon like peptide-1; GLF-1; GLF-2; parathyroid hormone; PTH; parathyroid hormone related hormone; adrenocorticotropic hormone, ACTH; pasepurin; esculetin; opioid peptide; gaegurin 5; agegurin; esculetin; opioid peptide; gaegurin 5; glucose dependent insulinotropic polypeptide; GIP; glucagon; motilin; thymposicin; biquitin; serum thymic factor; neurotrensin; tuffesin; gastrin; calcitonin; luteinising hormone releasing hormone; pancreatic polypeptide; amplin; corticotropin releasing factor; neuropeptide; amplin; galanin; somatostatic peptide; amplin; galanin; somatostatin; tutterin peptide; amplin; galanin; somatostatin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolytic polypeptide cleavage process useful for selectively cleaving the polypeptide at the Cys-His cleavage site, comprises solubilizing the polypeptide in a reaction mixture containing a palladium promoter dissolved in formic acid.
                           Amino acid sequence of chimeric protein T7tag-Vg-G5pr-CH-pth(1-34).
                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2003; 2003WO-US016647.
                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-2002; 2002US-0383484P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.6%;
Best Local Similarity 56.1%;
Matches 23; Conservative
06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REST-) RESTORAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seo JS, Holmquist B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-203533/19.
N-PSDB; ADJ87051.
                                                                                                                                                                                                                                                                                                                            WO2004011599-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 91 AA;
                                                                                                                                                                                                                                                                                                                                                           05-FEB-2004.
                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                 Chimeric
ij,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a palladium complex-promoted hydrolytic polypeptide cleavage process, which selectively cleaves the polypeptide at a Cyp-His cleavage site. The process comprises solubilising the polypeptide in a reaction mixture comprised of a palladium promoter dissolved in a high-concentration organic acid solvent. Also described: (1) a peptide purification process; and (2) a process for producing a peptide. The methods are useful for selectively cleaving the polypeptide at Cys-His cleavage site. The process provides a highly specific, conformationally independent, palladium promoted hydrolytic cleavage of polypeptides, including cleavage of relatively insoluble chimeric proteins in the form of inclusion bodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A palladium complex-promoted hydrolytic polypeptide cleavage process for cleaving the polypeptide at a Cys-His cleavage site, comprises solubilizing the polypeptide in mixture of a palladium promotor dissolved in organic acid solvent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                   palladium complex-promoted hydrolytic polypeptide cleavage; yet-His cleavage site; palladium promoter; chimeric protein; inclusion body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 103; DB 8; Length 91
Pred. No. 4.4e-05;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 IGGGGGG------GGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 VGGGGGPRCHSVSEIQLMHNLGRHLNSMERVEWLRKKLQDV 88
   AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
                     1 AVSEIGLMHNLGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; SEQ ID NO 19; 56pp; English.
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                                                                                                             ADF90346 standard, protein, 91 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strydom D, Holmquist B;
                                                                                                                                                                                                      Chimeric protein SEQ ID NO:19.
                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2003; 2003WO-US016468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 56.1%;
Matches 23; Conservative 1
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                                                                                                                                                                         26-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REST-) RESTORAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-053266/05.
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                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                          ADF90346;
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ADJ87052
ID ADJ8
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AC ADJ8
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The present sequence represents chimeric protein T7tag-Vg-G5pr-CH-pth(1-34). The protein comprises parathyroid hormone (PTH). The chimeric protein is used to demonstrate the process of the invention. The protein is used to demonstrate the process of the invention. The specification describes a hydrolytic polypeptide cleavage process which calcitively cleaves the polypeptide at the Cys-His cleavage site. The process comprises solubilising the polypeptide in a reaction mixture process comprises solubilising the polypeptide in a reaction mixture containing a palladium promoter dissolved in formic acid. The polypeptide is in the form of an inclusion body, and is preferably glucagon like peptide-1 (GLP-1), GLP-2, growth hormone related hormone, contendoration promone (ACTH), parathyroid hormone (PTH), parathyroid hormone (ACTH), enkephalins, endorphins, exendins, anylins, various opioid peptides, gaegurin 5, gaegurin 6, brevinin 1, collippides, dependent insulinotropic polypeptide (GIP), glucagon, motilin, thymopoietin, thymosin, ubiquitin, saturin, calcitonin, luteinish promone releasing factor, neuropeptide Y, arither process is highly specific, and is not intestinal paptide or insulin. The process is highly specific, and is not affected by the polypeptide or the size of the cleaved peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 103; DB 8; Length 91;
Pred. No. 4.4e-05;
1; Mismatches 3; Indels
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Claim 11; Fig 5; 41pp; English.
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Human parathyroid hormone analogue #65.
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                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                   Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a palladium complex-promoted hydrolytic polypeptide cleavage streeth which selectively cleaves the polypeptide at a Cys-His cleavage site. The process comprises solubilising the polypeptide in a reaction mixture comprised of a palladium promoter dissolved in a high-concentration organic acid solvent. Also described: (1) a peptide purification process; and (2) a process for producing a peptide. The methods are useful for selectively cleaving the polypeptide of Cys-His cleavage site. The process provides a highly specific, conformationally independent, palladium promoted hydrolytic cleavage of polypeptides, including cleavage of relatively insoluble chimeric proteins in the form of inclusion bodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A palladium complex-promoted hydrolytic polypeptide cleavage process for cleaving the polypeptide at a Cys-His cleavage site, comprises solubilizing the polypeptide in mixture of a palladium promotor dissolved in organic acid solvent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                         palladium complex-promoted hydrolytic polypeptide cleavage;
Cys-His cleavage site; palladium promoter; chimeric protein;
inclusion body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 141;
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                                                                           ADF90348 standard; protein; 141 AA
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                                                                                                                                                                 Chimeric protein SEQ ID NO:21
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56.1%;
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                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (REST-) RESTORAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-053266/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Strydom D,
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                                                                                                                                     26-FEB-2004
                                                                                                                                                                                                                                                                                                                 04-DEC-2003
                                                                                                                                                                                                                                                        Synthetic.
    48
                                                                                                        ADF90348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New parathyroid hormone analogs, used for treating e.g. abnormal CNS or pancreatic functions, abnormal mineral metabolism and homeostasis, male infertility, abnormal blood pressure or hypothalmic disease.
Human, parathyroid hormone, parathyroid hormone-related protein; PTH; PTHP; analogue; abnormal CNS function, pancreatic function; mineral metabolism; male infertility; abnormal blood pressure; hypothalmic disease.
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                                                                                                                                                                                                                                                    /label= OTHER
/note= "OTHER=cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "OTHER=cyclohexylalanine"
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note= "OTHER=des-Asn"
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                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             label= OTHER
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71.0%;
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                                                                                                                                                                                                                              Modified-site
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This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism
                                                           Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Target peptide (PTH(1-38)) used in fusion protein construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.7%; Score 100; DB 2; Length 38; llarity 74.2%; Pred. No. 4.4e-05; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pusion protein construct, isolation, purification, growth hormone releasing factor; glucagon-like peptide 1. parathyroid hormone, inclusion body; carbonic anhydrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rainer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVSEIQLMHNLGGHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                           Waelchli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 101; Page 39; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR98958 standard; peptide; 38 AA.
                                                                                                                                                                                                                                                                  92GB-00026415.
92GB-00026859.
92GB-00026861.
93GB-00001691.
93GB-00007673.
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20-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis I, Schneider H,
                               [Gly13] -hPTH (1-38) -OH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-018352/03.
                                                                                                                                                                                                                                                                                                                                                                                                         (SANO ) SANDOZ LTD.
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38 AA;
                                                                                                                                                                                                                                                                    18-DEC-1992;
23-DEC-1992;
23-DEC-1992;
28-JAN-1993;
14-APR-1993;
19-APR-1993;
                                                                                                                                                                                                                      12-JUL-1993;
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                                                                                                                                                                                      02-FEB-1994.
                                                                                                                                                     GB2269176-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR98958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of parathyroid hormone (PTH) or parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2 receptor agonists or antagonists and can be used in the treatment of disorders resulting from allered or excessive action of the PTH2 receptor, e.g. abnormal CNS functions, abnormal pancreatic functions, divergence from normal mineral metabolism and homeostasis, male infertility, abnormal blood pressure or a hypothalmic disease. The present sequence is a peptide analogue of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New parathyroid hormone analogs, used for treating e.g. abnormal CNS or panoreatic functions, abnormal mineral metabolism and homeostasis, male infertility, abnormal blood pressure or hypothalmic disease.
                                                                                             Human, parathyroid hormone, parathyroid hormone-related protein, PTH, PTH+P; analogue, abnormal CNS function, pancreatic function; maineral metabolism; male infertility; abnormal blood pressure; hypothalmic dieses.
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                                                                                                                                                                                                                                                                      /label= OTHER
/note= "OTHER=cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                           'note= "OTHER=cyclohexylalanine"
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                                                                 Human parathyroid hormone analogue #33.
                                                                                                                                                                                                                                                                                                                        OTHER "OTHER=des-Met"
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                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR58104 standard; peptide; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 39; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                           label= OTHER
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                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-038790/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34 AA;
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Modified-site
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                                                                                                                                                                                      Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9957139-A2
                                   02-DEC-2002
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   ABJ10737;
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Gaps

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95WO-US015800

07-DEC-1995;

AAR58104;

RESULT 11
AARS8104
ID AARS8
XX
AC AARS8

Best Loc Matches

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1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
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22-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues 35-84 may be absent. The C-terminal gp. may be -COOH, -COO-+M (M+ = cation), or -(C=O)MH2. 140 specific peptides derived from human PTH are given in the specification (AAR21150-256, AAR23226- 3250 + AAR23522-
                                                                                                                                                                  peptide employs a fusion protein construct (FPC) comprising a carbonic anhydrase and a variable fused polypeptide containing a target peptide. The method comprises precipitating either the FPC or a fragment of FPC including the carbonic anhydrase. An alternative method of producing the peptide comprises expressing the FPC as part of an inclusion body. The target peptides of the FPC are derived from growth hormone releasing factor (GRF), glucagon-like peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence corresponds to amino acids 1-38 of PTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified parathyroid hormone analogues - useful in treating cancer, osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
                                                    De La Motte RS;
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                      Isolation and purificn of peptide(s) from fusion protein constructs which include a carbonic anhydrase and a variable fused polypeptide
                                                                                                                                                         method for the isolation and/or purification of a recombinant
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                                                                                                                                                                                                                                                                                    Length 38;
                                                                                                                                                                                                                                                                                                       Indels
                                                    Manning SD,
                                                                                                                                                                                                                                                                                             Pred. No. 4.4e-05;
1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human parathyroid hormone analogue, [Gly6]hPTH.
                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                             1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTH; agonist; antagonist; receptor binding.
                                                    Henriksen DB,
                                                                                                                                                                                                                                                                                     Score 100;
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                                                                                                                                                                                                                                                                                                                                                                                                     AAR21168 standard; protein; 84 AA
                                                                                                                                     Claim 58; Page 50; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 64; 86pp; English
                                                                                                                                                                                                                                                                                    61.78;
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           94US-00350530
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(first entry)
                                                                                                                                                                                                                                                                                             Local Similarity 74.2
nes 23; Conservative
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                                                    Stout JS,
Wagner FW;
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                                (BION-) BIONEBRASKA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-056643/07.
                                                                                 WPI; 1996-287186/29
                                                                                                                                                                                                                                                                Sequence 38 AA;
                                                    Partridge BE,
Holmquist B,
           07-DEC-1994;
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17-JUN-1992
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                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                  ö
PTH are also claimed. All have mutations at positions 3, and/or 6, and/or 9 which result in surface side chains which are useful to modulate receptor binding and activity. They are useful as agonists and antagonists in the treatment of condi- tions or diseases involving PTH. The peptides are pref. prepd. by solid phase synthesis. See also AAR21257 (human generic), AAR21258 (bovine generic) and AAR21259 (porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified parathyroid hormone analogues - useful in treating cancer, osteoporosis, hypercalcaemia and hyper-parathyroid conditions.
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                                                                                                                                                                                                                                                                                                                    Score 100; DB 2; L
Pred. No. 9.6e-05;
1; Mismatches 7;
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Pred. No. 0.00013
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVSEIGLMHNLGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
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74.2%;
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74.2%;
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 74.28
Marches 23, Conservative
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nes 23; Conservative
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The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1.34 in which at least one of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 is cyclohexylalanine (Cha). In this example the Leu residue at position 7 and the Leu at position 11 in the wild-type have been substituted by Cha. The hPTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin). N.B. The present sequence does not appear in the modification. It corresponds to the known hPTH 1.34 fragment with the modifications as stated in the claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and bone fracture.
                                                                                                                                                                              Osteoporosis; agonist; PTH; human; anti-resorptive therapy; bone fracture.
                                                                                                                                                       Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.
                                                                                                                                                                                                                                                                                    /
/label= OTHER
/note= "Cyclohexylalanine (Cha)"
/note= "In amide form"
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                              AAW17939 standard; peptide; 34 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0001105P.
95US-0003305P.
96US-00626186.
                                                                                                                                                                                                                                                                                                                             /label= OTHER
/note= "Cha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US011292.
                                                                                                                               29-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-118819/11.
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Modified-site
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06-SEP-1995;
29-MAR-1996;
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                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
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                                                     RESULT 15
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0; Gaps

Query Match 60.5%; Score 98; DB 2; Length 34; Best Local Similarity 71.0%; Pred. No. 6.9e-05; Matches 22; Conservative 1; Mismatches 8; Indels

qq

Search completed: November 21, 2005, 16:10:12 Job time : 142.5 secs

Fri

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein November 21, 2005, 16:05:13 ; Search time 23.5 Seconds Run on:

(without alignments) 126.924 Million cell updates/sec

US-09-475-158A-5 162 1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31

**BLOSUM62** Scoring table: Sequence:

Perfect score:

283416 seqs, 96216763 residues Searched:

Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries \*:08 Database :

pir1:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	parathyroid hormon	ABC transport prot	related to proline	transcription fact	early growth respo	myc far upstream e	probable DNA bindi	regulatory protein	probable protein p	neurogenic locus m	1-phosphatidylinos	endo-1,4-beta-xyla	hypothetical prote		hypothetical prote	AcrB/AcrD/AcrF fam	hypothetical prote	hypothetical prote	acp-22 protein - y	acp-22 protein - y	hypothetical prote	protein F17L21.18	ein trihel	hdc protein - frui					
	ΩI	PTHU	PTBO	JC4202	PTPG	A05091	151851	T18288	T49559	S71795	A41211	A53184	T03605	A41696	T13926	A33106	T18273	140712	T45737	C96699	D96664	G87398	G84746	T49450	S16063	S32224	T49792	D86399	B86456	S58064
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٠,	Query Match	56.8	56.2	54.3	51.9	47.5	44.4	40.7	39.5	39.5	39.5	39.2	38.9	38.9	38.9	38.9	38.9	38.6	38.3	38.3	38.0	38.0	38.0	37.7	37.7	37.7	37.7	37.7	37.7	37.7
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1 2 A35912 7 2 S57795 9 2 T41868 9 2 T06612 0 2 T20961 0 2 T20961 1 2 F84596 0 2 A42687 0 2 A42687 7 2 A60643 6 2 T49109 3 1 S29334 5 1 S31224	671 2 A35912 239 2 S57795 239 2 S49193 315 2 T41868 339 2 T06612 570 2 T27407 455 2 B86427 201 2 P84596 210 2 A46179 287 2 A60643 396 2 T49109 433 1 S29334 445 1 S31224	homeotic protein o	probable deoxyribo	GCR 101 protein -	hypothetical prote	glycine-rich prote	neurotrophin-4 pre	U2 BRRNP auxiliary	antigen 5401 - Eim	glycine-rich prote	UL44 protein - hum	transcription fact	transcription fact				
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parathyroid hormone precursor [validated] - human
NyAlternate names: proparathyroid hormone
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence\_revision 19-Jan-1996 #text\_change 09-Jul-2004
C;Accession: A19339; S53790; A33169; S21199; A33789; A93783; A93787; A90486; A94410; I38
R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., USroc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
A;Title: Nuclectide sequence of the human parathyroid hormone gene.
A;Reference number: A19339; MUID:83169834; PMID:6220408

A;Molecule type: DNA A;Residues: 1.115 «VAS. A;Grossa-references: UNIPROT: PO1270; UNIPARC: UPI000013290A; GB:J00301; NID:g190702; PIDN R;Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K. Biol. Chem. Hoppe-Seyler 375, 821-824; 1994 A;Title: Purification of meprin from human kidney and its role in parathyroid hormone d∈ A;Reference number: S53790; MUID:95225988; PMID:7710697

A; Accession: S53790

A; Molecule type: protein
A; Reaidues: 'X', 33, 'X', 35-46;65-84;105-110 <YAM>
A; Reaidues: 'X', 33, 'X', 35-46;65-84;105-110 <YAM>
A; Cross-references: UNIPARC: UP100001734E1; UNIPARC: UP100001734E2; UNIPARC: UP100001734E3
A; Orde: peptides generated in vitro and in vivo by meprin; peptide cleavage also occurr
R; Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974
A; Title: Structural analysis of human proparathyroid hormone by a new microsequencing a;
A; Reference number: A93169; MUID: 74174967; PMID: 4833516

A;Accession: A93169 A;Molecule type: protein A;Residues: 26-37 <JAC.> A;Cross-Acences: UNIPARC:UPI00001734E4 A;Cross-Acences: UNIPARC:UPI00001734E4 R;Olstead, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik, V.: Eur. J. Biochem. 205, 311-319, 1992

A, Title: Isolation and characterization of two biologically active O-glycosylated forms

A;Reference number: S21199; MUID:92209518; PMID:1555591

A; Accession: S21199

A; Molecule type: protein
A; Residues: 32-114, 7N' <0LS>
A; Residues: 32-114, 7N' <0LS>
A; Residues: 32-114, 7N' <0LS>
A; Cross-rences: UNIPARC: UPI00001734ES
A; Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation
R; Niall, H.D.; Sauer, R.T.; Jacoba, J.W.; Keutnann, H.T.; Segre, G.V.; O'Riordan, J.L.H
Proc. Natl. Acad. Sci. US.A. 71, 384-388, 1974
A; Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid
A; Reference number: A93789; MUID:74111656; PMID:4521809

A, Accession: A33789
A, Molecule type: protein
A, Residues: 32-68 < NIA>
A; Cross-references: UNIPARC: UP1000002DA05
A; Cross-references: UNIPARC: T, Ronan, R.; Sizemore, G.W.; Arnaud, C.D. Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

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A;Molecule type: mRNA
A;Residues: 1-115 <WED.
A;Crosd.references: UNIPARC:UPI0000132907; GB:J00024; NID:g163642; PIDN:AAA30747.1; PID
R;Weaver, C.A.; Gordon, D.F.
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Csuperfamily: parathytoid hormone, parathyroid gland; hormone homology
C; Superfamily: parathytoid djand; plasma
C; Eywords: calcium; hormone; parathyroid gland; plasma
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-31/Domain: propeptide #status experimental <RRO>F;30-64/Domain: parathyroid hormone homology <PTH>F;32-115/Product: parathyroid hormone #status experimental <MAT>
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56.8%; Score 92; DB 1; Length 115;
Best Local Similarity 71.0%; Pred No. 0.00047;
Matches 22; Conservative 1; Mismatches 8; Indels

Matches 22; Conservative 1; Mismatches 8; Indels
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A; Molecule type: protein
A; Mesidues: 26-115 - CCHD: A CCHD: A; C
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A; Residues: 32-109 <SAU>
A; Residues: 32-109 <SAU>
A; Cross-references: UNIPARC:UPI00001734E0
A; Cross-references: UNIPARC:UPI00001734E0
Am. J. Med. 55, 759-766, 1974
Ajrill: Recent studies on the chemistry of human, bovine and porcine parathyroid hormor
A; Reference number: A90030; MUID:74173303; PMID:4598526
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A,Residues: 1-115 <HEIT
A,Residues: 1-115 <HEIT
A,Residues: 1-115 <HEIT
A,Residues: 1-115 <HEIT
A,Notes-references: UNIPARC:UPI000013290C; GB:K01268; NID:g206483; Pl
A,Notes: the authors translated the codon GAA for residue 87 as Asp
R,Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res: 15, 6740, 1987
Nucleic Acids Res: 15, 6740, 1987
A,Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid A,Reference number: A26806; MUID:87316938; PMID:3628009
                             A,Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial A;Reference number: A90390; MUID:76018954; PMID:1164500
A;Accession: A90390
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05091; A26806
R;Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
R;Heinrich, G.; Kronenberg, 1984
A;Reference number: A05091; MUID:84135846; PMID:6321505
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C; Superfamily: parathyroid hormone; parathyroid dland

C; Superfamily: parathyroid parathyroid gland

C; Seywords: calcium; hormone; parathyroid gland

P;1-25/Domain: signal sequence #status predicted <SIG>

P;26-31/Domain: propeptide #status experimental <PRO>

P;30-64/Domain: parathyroid hormone homology <PTH>

F;32-115/Product: parathyroid hormone #status experimental <PAT>
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64.5%; Pred. No. 0.0041;
iive 3; Mismatches
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Pred. No. 0.028;
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C; Superfamily: F; 30-64/Domain:
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Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
A;Reference number: 145976; MUID:83105964; PMID:6185374
A;Accession: 145976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Cross-references: UNIPARC:UPI0000132907; GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:
C;Genetics:
A;Gene: PTH
A;Introns: 29/2
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Keywords: hormone
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-115/Product: propertide #status experimental <PMAT>
F;26-115/Product: parathyroid hormone #status experimental <PMAT>
F;30-64/Domain: parathyroid hormone #status experimental <PMAT>
F;31-115/Product: parathyroid hormone #status experimental <MAT>
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C; Species: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C; Species: Lo. Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C; Accession: JC4202
R; Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.C.
Gene 160, 241-243, 1995
A; Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein and
A; Reference number: JC4202
A; Molecule type: mRNA
A; Residues: L-115 < ROS>
A; Cross-references: UNIPROT:P52212; UNIPARC:UPI0000132908; GB:U15662; NID:G558915; PIDN:
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C; Keywords: hormone
F;1-31/Domain: signal sequence #status predicted < SIG>
F;30-64/Domain: parathyroid hormone homology < PTH>
F;32-115/Product: parathyroid hormone #status predicted < NAT>
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: B26806, A90390; A90376; A0153
R;Schmelzer, H.J.; Gross, G; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: B26806
A;Cross-reference: UNIPROT:P01269; UNIPARC:UPI000013290B; GB:X05722; GB:Y00409; NID:918
B;Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 115;
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Best Local Similarity 71.0%; Pred. No. 0.00062;
Matches 22; Conservative 1; Mismatches 8;
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Best Local Similarity
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571795
Franscription factor CBF-2 - chicken
C;Species; Gallus gallus (chicken)
C;Species; Gallus gallus (chicken)
C;Accession: S71795
Fridas, J; Hirano, S; Yamagata, M.; Noda, M.
Nature 382, 632-635, 1996
A;Title: Visual projection map specified by topographic expression of transcription facto.
A;Accession: S71795
A
                                                                                                              Ouery Match 39.5%; Score 64; DB 2; Length 212; Best Local Similarity 45.8%; Pred. No. 1.7; Matches 11; Conservative 5; Mismatches 8; Indels
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Pred. No. 3.5;
1; Mismatches 1
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Best Local Similarity 84.6
Matches 11; Conservative
A; Map position: 6
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118.28B
TIB 18.28
TIB 28
T
                                                                                               Jarshy Mormone - rat (fragment)
parathyroid hormone - rat (fragment)
parathyroid hormone - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: 151851
R;Schmedzer, H. .
A;Title: Nucleocide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A;Title: Nucleocide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A;Accession: 151851
A;Accession: 151851
A;Accession: 151851
A;Accession: 151851
A;Accession: 151852
A;Accession: 151852
A;Accession: 151852
A;Coss-references: UNIPARC:UP10000170AE0; GB:M54875; NID:g601932; PIDN:AAA57156.1; PIDD:C;Genetics:
C;Genetics: PTH
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;20-54/Domain: parathyroid hormone homology < PTH>
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44.4%; Score 72; DB 2;
Best Local Similarity 56.7%; Pred. No. 0.098;
Matches 17; Conservative 4; Mismatches
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A,Title: nit-4, a pathway-specific regulatory gene of Neurospora crassa, encodes a prote
A,Reference number: A41696, MUID:92017855, PMID:1840634
A,Accession: A41696
                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-99,'P',99-466,'S',468-1090 <YU2>
A;Cross-references: UNIPARC:UP10000168940; EMBL:M80368; NID:g168848; PIDN:AAA33602.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1428 - DLC>
A;Cross-references: UNIPROT:O77023; UNIPARC:UPI000007E714; EMBL:U96697; NID:g3403155; Pi
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NyAlternate names: mastermind protein
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: A36391, A33106; E13514
R;Smoller, D.; Friedel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B.
A;Smoller, D.; Friedel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B.
A;Title: The Drosophila neurogenic locus mastermind encodes a nuclear protein unusually
A;Reference number: A36391, MUID:91065516; PMID:1701150
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                                                                                                                       A;Residues: 1-1090 <YUA>
A;Cross-references: UNIPROT: P28349; UNIPARC: UPI00001301D7; GB:M80368
R;Yuan, G.F.; Fu, Y.H.; Marzluf, G.A.
Bubmitted to the EMBL Data Library, December 1991
A;Description: nit-4, a pathway-specific regulatory gene of Neurospora crassa, A;Reference number: S37629
A;Accession: S37629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable protein phospharase 2C1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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C;Keywords: DNA binding; nucleus; transcription regulation; zinc finger
F;48-86/Domain: GAL4 zinc binuclear cluster homology <GAL4>
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Pred. No.
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A,Cross-references: FlyBase:FBgn0022768
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| AAGRVGGGGGGGGRGS 1140
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Query Match
Best Local Similarity 48.09
Matches 12; Conservative
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A; Residues: 1-1596 <SMO>
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Best Local Similarity
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R;Nakase, M; Aoki, N; Matsuda, T.; Adachi, T.
Plant Woll. Biol. 33, 513-522, 1997
A;Title: Characterization of a novel rice bZIP protein which binds to the alpha-globulin A;Reference number: Z14974; MUID:97201485; PMID:9049271
A;Accession: T03605
A;Accession: T03605
A;Greence reliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-425 <NAKA
A;Crosse-references: UNIPROT:P93405; UNIPARC:UPI00000A1985; EMBL:D78609; NID:g1122224; PI
A;Experimental source: subsp. Japonica, cv. Nipponbare, endosperm
C;Superfamily: BZIP protein; fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myc far upstream element-binding protein - human
NyAlternate names: FUSE-binding protein
NyAlternate names: FUSE-binding protein
NyAlternate names: FUSE-binding protein
C.Species: Namo sapiens (man)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C,Accession: A53184
R:Duncan, R: Bazar, L: Michelotti, G:; Tomonaga, T:; Krutzsch, H.; Avigan, M.; Levens, Genes Dev. 8, 465-480, 1994
A;Itle: A sequence-specific, single-strand binding protein activates the far upstream e A;Accession: A53184
A;Reference number: A53184
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-644 cDUN>
A;Residues: 1-644 cDUN>
A;Residues: 1-644 cDUN>
A;Cross references: UNIPARC:UPI000017C2AF; GB:U05040; NID:g460151; PIDN:AAA17976.1; PID: C;Keywords: DNA binding
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C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 31-Dec-2004
C;Accession: A41696, S37629; $20033
R;Yuan, G.F.; Fu, Y.H.; Marzlut, G.A.
Mol. Cell. Biol. 11, S735-S745, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable DNA binding protein - rice
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
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                                                                              39.5%; Score 64; DB 2; Length 543; 80.0%; Pred. No. 4.3; tive 0; Mismatches 3; Indels
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           F;340-419/Domain: DNA binding #status predicted <DNB:
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A;Cross-references: UNIPROT:P21519; UNIPARC:UPI000012EB74; GB:X54251; NID:g8203; PIDN:CA A;Note: strain Canton S Genetics: C;Genetics: A;Gene: FlyBase:mam A;Cross-references: FlyBase:FBgn0002643
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                                                                                                                            Query Match

38.9%; Score 63; DB 2; Length 1596;
Best Local Similarity 84.6%; Pred. No. 16;
Matches 11; Conservative 1; Mismatches 1; Indels
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354 VGGGGGGGGGNS 366
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November 21, 2005, 15:55:27; Search time 146.5 Seconds (without alignments) 149.293 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV
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Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters: seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

2166443 segs, 705528306 residues

Searched:

2166443

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	P01270 homo s	Q9xt35		P01268	Q9nlv0 equus	FA P52212 cani	P01269 sus sc	09g16	AT	P04089	OUSE Q9201	P53349 mus mu	Q6k708 oryza	Q6t5k2		Q785u3	Q4idd8	Q5krj6	Q81n95	Q6pf28 xenopu	Q94h89 oryza	069117	073627	Q5n802	Q7pyh7		CRYNE Q5kgh1	BDEBA Q6mjt1	059mn	0785t5	11 - 17 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1
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# ALIGNMENTS

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
MEDLINE=82150870; PubMed=6950381;
Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;
"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE OF 32-68.
MEDLINE=7411656, PubMed=4521809,
Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
Niall H.D., Aurbach G.D., Potts J.T. Jr.,
"The amino-acid sequence of the amino-terminal 37 residues of human
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G.N.
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WUCLEOTIDE SEQUENCE.

WICLINE=83169834; PubWed=6220408;

Wasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J., Hendy 'Vasicek T.J., McCevitt B.E., Freeman M.W.,

Potts J.T. Jr., Rich A., Kronenberg H.M.;

Wucleotide sequence of the human parathyroid hormone gene.";

Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
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PROTEIN SEQUENCE OF 26-40.
PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
                                                           21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T., "Structural analysis of human proparathyroid hormone by a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [6]
PROTEIN SEQUENCE OF 61-83 AND 84-115.
MEDLINE=79082855; PubMed=728431;
Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,
                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981)
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                              115 AA
                              PRT;
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MEDLINE=74174967; PubMed=4833516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microsequencing approach.";
Nature 249:155-157(1974).
                              STANDARD;
                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                               NCBI_TaxID=9606;
                                PTHY_HUMAN
                                                                                                                                 Name=PTH
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RESULT 1
PTHY HUMAN
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SIGNAL
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PERUCTURE BY NMR OF 32-65.
MEDIATE-9199748; Pubmed=2069952;
KIDLURE-9199748; Pubmed=2069952;
KIDLUR W. Dieckmann T., Waray V., Schomburg D., Wingender E., Mayer H.;
"Investigation of the solution structure of the human parathyroid hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and molecular dynamics calculations.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRUCTURE BY NMR OF 32-70.
MEDLINE-2006619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
MARY U.C., Adermann K., Bayer P., Foresmann W.-G., Rosch P.;
"Solution structures of human parathyroid hormone fragments hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
Blothem. Blothyr. Res. Commun. 267:213-220(2000).
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MEDLINE=75146516; PubMed=1125201;
Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
"A reinvestigation of the amino-terminal sequence of human parathyroid
                                                                                                                                                                                                                                  NEUTHESIS OF 32-65.
MEDILINE=7505920; PubMed=4474131;
MEDILINE=7505920; PubMed=4474131;
Pregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T.,
Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
"Solid-phase synthesels of the biologically active N-terminal 1-34
peptide of human parathyroid hormone.";
Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
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MEDILINE-55318064, Pubmed-1797503, DOI=10.1074/jbc.270.25.15194,
MEDILINE-55318064, Pubmed-n. S. Bayer P., Adermann K., Ejchart A.,
Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
                                      [7]
PROTEIN SEQUENCE OF 75-100.
Keutemann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N., O'Riordan J.L.H., Potts J.T. Jr.;
O'Riordan J.L.H., Potts J.T. Jr.;
Cin) Talnadge R.V., Owen M., Parsons J.A. (eds.);
Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation, Amgterdam (1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NWR OF 32-65.
MEDLINE-93345518; PubMed-8344299;
Barden J.A., Cuthbertson R.M.;
"Stabilized NMR Structure of human parathyroid hormone(1-34).";
Eur. J. Biochem. 215:315-321(1993).
             of human parathyroid hormone.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WARIANT FIH ARG-18.
MEDLINE=91009811; PubMed=2212001;
MEDLINE=91009811; PubMed=2212001;
MEDLINE=91009811; PubMed=2212001;
Kronenberg H.M.;
"Mutation of the signal peptide-encoding region of the preproparathyroid hormone gene in familial isolated
                                                                                                                                                                                                                                                                                                                                        SYNTHESIS OF 32-65.

Madreatta R.H., PubMed=4721748,

Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
Riniker B., Rittel W., Sieber P.,

Synthesis of sequence 1-34 of human parathyroid hormone.",
Helv. Chim. Acca 56:470-473 (1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypoparathyroidism.";
J. Clin. Invest. 86:1084-1087(1990)
                                                                                                                                                                                "A reinvesciss".
hormone ";
Biochemistry 14:1842-1847(1975).
 Potts J.T. Jr.;
"Complete amino acid sequence o
Biochemistry 17:5723-5729(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [16]
VARIANT FIH PRO-23.
PubMed=10523031;
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Annowed magnetic properties of the signal groups of the preproparative production and annowed magnetic processive familial isolated by the signal segment of the segment of the signal segment of the segment of the signal ```

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MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Lischul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,

A Brapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Agribos R.A.,

A Pahey J., Hellon B., Schergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Hallon B., Scheman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimmood J.W., Green E.D., Dickson M.C.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

A Generation and initial analysis of more than 15,000 full-length human
                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lauraaiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
   TISSUE=PCR rescued clones;
NIH MGC Project;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
  115 AA; 12861 MW; 849015736A6E5597 CRC64;
   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
  Score 92; DB 2; Le
Pred. No. 0.0031;
1; Mismatches 8;
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62
  PRT; 115 AA
  InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR003625; Pthyrhorm_sub.
Pfam; PF01279; Parathyrd.
  EMBL; BC096143; AAH96143.1; -; mRNA.
EMBL; BC096144; AAH96144.1; -; mRNA.
   EMBL; BC096145; AAH96145.1; -; mRNA.
EMBL; BC096142; AAH96142.1; -; mRNA.
  Pfam; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
ProDom; PD010687; Pthyrhorm_eub; 1.
  PROSITE; PS00335; PARATHYROID; 1.
SEQUENCE 115 AA; 12861 MW; 84
   [1]
NUCLEOTIDE SEQUENCE.
MEDLINE=80056617; PubMed=388425;
   56.8%;
71.0%;
   IISSUE=PCR rescued clones;
  22; Conservative
   STANDARD;
   SMART; SM00087; PTH;
   Bos taurus (Bovine).
sapiens (Human)
   NUCLEOTIDE SEQUENCE
  Local Similarity
   NCBI_TaxID=9913;
   NCBI_TaxID=9606;
   PTHY_BOVIN
ID PTHY_BOVIN
AC P01268;
  Name=PTH;
  32
  Query Match
  Matches
   RESULT
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  IN SECOND   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                   ö
   Gaps
   MUCLEOTIDE SEQUENCE.
Malaivijitnond S., Takenaka O.;
Malaivijitnond S., Takenaka O.;
Malaivijitnond S., Takenaka O.;
Intaliand.";
J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
I. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
I. FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
I. SUBCELLULAR LOCATION: Secreted.
I. SUBCELLULAR LOCATION: Secreted.
                                   Gaps
   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
Cercopithecidae, Cercopithecinae; Macaca.
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                                   ö
   Ouery Match 56.8%; Score 92; DB 1; Length 115; Best Local Similarity 71.0%; Pred. No. 0.0031; Matches 22; Conservative 1; Mismatches 8; Indels
                                   Indels
   1 25 By similarity.
26 31 By similarity.
32 115 Parathyroid hormone.
115 AA: 12890 MW; 8C2500EF24BE5597 CRC64;
   13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Parathyroid hormone, preproprotein.
                                ..
  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
No. 0.0031;
   115 AA
  115 AA
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 62
   EMBL; AF130257; AAD42777.1; -; Genomic_DNA.
HSSP; P01270; 1ET1.
      Pred. No. 0.00
1; Mismatches
  nicerpro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Pehyrhorm sub.
PANTHER; PTHR10541; Pthyrhorm sub; 1.
Pfan; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
  ProDom, PD010687; Pthyrhorm sub; 1. SMART; SM00087; PTH; 1. PROSITE; PS00335; PARATHYROID; 1.
  PRT;
71.0%;
   Q4VB48 HUMAN PRELIMINARY;
Q4VB48;
                                22; Conservative
  STANDARD;
         Similarity
  Hormone; Signal.
  NCBI_TaxID=9541;
  MACFA
   SEQUENCE
  Name=PTH:
  RESULT 3

Q4VB48 HUMAN

1D Q4VB48 HU

Q4VB48 HUMAN

D1 13-SEP-20

D1 13-SEP-20

D1 13-SEP-20

D2 Parathyro

GN Name=PTH
      Best Local
   removed
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   MACFA
                                      Matches
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  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Inseltute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
   [9]

STRUCTURE BY NMR OF 32-68.

MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

Marx U.C., Adermann K., Bayer P., Forsemann W.-G., Rosch P., Forsemann Schophys. Res Commun. 267:213-220(2000)

Blochem Biophys. Res commun. 267:213-220(2000)

Forsemann Biophys. Res commun. 267:213-220(2000)

Forsemann Biophys. Reserve acicium level by dissolving the salts in bone and preventing their renal excretion.

-1. SUBCELLULAR LOCATION: Secreted.

-1. SIMILARITY: Belongs to the parathyroid hormone family.
   [5]
PROTEIN SEQUENCE OF 26-115.
MEDIINE-74142666; PubMed=4522780;
Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
Cohn D.V.;
"The N-terminal amino-acid sequence of bovine proparathyroid
Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A., Potts J.T. Jr., Rich A.;
Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid hormone.";
Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
  SYNTHESIS OF 32-65.
MEDLINE-T1991S8; PubMed=4122265;
MEDLINE-T1991S8; PubMed=4122265;
MEDCHG J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
Synthesis of a blologically active N-terminal tetratriacontapeptide
of parathyroid hormone. "P. G. 68:63-67(1971).
  MEDLINE-82037785; PubMed=6170060; Weaver C.A., Gordon D.P., Kemper B.; Waver C.A., Gordon D.P., Kemper B.; Weaver C.A. Introduction by molecular cloning of artifactual inverted seguences at the S' terminus of the sense strand of bovine parathyroid hormone
   NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
MEDLINE=81105964; PubMed=6185174; DOI=10.1016/0303-7207(82)90136-8;
Weaver C.A., Gordon D.F., Kemper B.;
Waver C.A., Gordon D.F., Kemper B.;
Waver C.B., Gordon D.F., Kemper B.;
Watleotide sequence of bovine parathyroid hormone messenger RNA.";
Mol. Cell. Endocrinol. 28:411-424(1982).
  [4]
MEDLINE-8426483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
"Isolation and complete nucleotide sequence of the gene for bovine
   PROTEIN SEQUENCE OF 32-115.

MEDLINE=71076162, Pubmed=5531031;

Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
Autabed G.D., Potte J.T., Jr.,
The amino acid sequence of bovine parathyroid hormone I.";
Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
HOPPE-SEYLER'S Z. Physiol. Chem. 351:1586-1588(1970).
PROTEIN SEQUENCE OF 32-115.
MEDLINE=71063634; Pubmed=5275384;
Brewer H.B. Jr., Roman R.,
Brower H.B. Jr., Roman R.,
Brower H.B. Jr., Roman R.,
Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
   Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981)
   Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974)
   parathyroid hormone.";
Gene 28:319-329(1984).
   NUCLEOTIDE SEQUENCE
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Gaps
   who would be appended as a control of the control o
   Equus caballus (Horse).

Equus caballus (Horse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euteria; Laurasiatheria; Perissodactyla; Equidae; Equus.
   NUCLECTIDE SEQUENCE.
MEDILINE-200829-17: PubMed=10613847; DOI=10.1101/gr.9.12.1239;
MEDILINE-200829-17: PubMed=10613847; DOI=10.1101/gr.9.12.1239;
Cacteano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
Bowling A.T., Murray J.D.;
"A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1239-1249(1999).
   .
0
EMBL; V00106; CAA23439.1; -; mRNA.
EMBL; V00204; AAA30747.1; -; mRNA.
EMBL; K01038; AAA30749.1; -; Genomic_DNA.
EMBL; M01038; AAA30749.1; -; Genomic_DNA.
EMBL; M01038; AAA30749.1; -; mRNA.
ENEL; M20508; AAA30748.1; -; mRNA.
PIR; A24349; PFR 06.32-68.
INTEAPO; IPR001415; Parathyrd_hrm.
INTEAPO; IPR0013035; PTHYNOTM_sub.
PANTHER; PTHR10541; PEHYRHORM_sub; 1.
PFR590139; PARTHYROTM, PHYTHYROTM, PHYTHYRO
   56.2%; Score 91; DB 1; Length 115; 71.0%; Pred. No. 0.0041; cive 1; Mismatches 8; Indels
   63
12980 MW; 2ED246B348880710 CRC64;
   9805 MW; 253184EA681A2022 CRC64;
  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Parathyroid hormone (Fragment)
   Parathyroid hormone V -> G (in Ref. 4).
   86 A.A.
  32 AVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62
  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
  PRT;
  SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
   Query Match
Best Local Similarity '-
22, Conservative
  Q9N1VO_HORSE PRELIMINARY;
   1115
106
40
42
52
50
  NUCLEOTIDE SEQUENCE.
  26
32
106
37
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51
51
115 AA;
  86 AA;
   NON TER
SEQUENCE
   CHAIN
CONFLICT
HELIX
   SEQUENCE
  HORSE
   09N1V0
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   HID DATA DATA BENERAL ```

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115 AA

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PROTEIN SEQUENCE OF 32-115.

MEDLINE-4253317; PubMed-4840833;
Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
Potts J.T. Jr.,
"The amino acid sequence of porcine parathyroid hormone.";
"The Biochemistry 13:1994-199911974).
-i- FUNCTION: PTH elevates calcium level by dissolving the salts in
                                                                                                              Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Butheria; Laurasiatheria, Cetartiodactyla; Suina, Suidae;
                                                                                                                                                                                                                                                                                                   MEDLINE=76018954; PubMed=1164500;
Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
Porchie proparathyroid hormone. Identification, biosynthesis, and
partial amino acid sequence.";
Biochemistry 14:3631-3635(1975).
                                                                                                                                                                                              MEDLINE=87316938; PubMed=3628009; Schmelzer H.-J., Gross G., Widera G., Mayer H.: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat."; Nucleic Acids Res. 15:6740-6740(1987).
            21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH)
Name=PTH;
                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE OF 26-115
STANDARD;
                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    removed.
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                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Capen C.C.; "Sequences of the cDNAs encoding canine parathyroid hormone-related protein and parathyroid hormone."; Gene 160:241-243(1995).
                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95369696; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C;
                                                                                                                                                                                                                                                                                                                                                                                                            Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- FUNCTION: FTH elevates calcium level by dissolving the salts bone and preventing their renal excretion.
-:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 115;
               Query Match 54.3%; Score 88; DB 2; Length 86; Best Local Similarity 67.7%; Pred. No. 0.0069; Matches 21; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 By similarity.
31 By similarity.
115 Parathyroid hormone.
12957 MW; FC338F77F1C8CFE56 CRC64;
                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensempl; ENSCAFGO000008177; Canis familiaris.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR001415; Parathyrdorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
Pfam; PF01279; Parathyroid; 1.
ProDom; PD010687; PTH; 1.
PROSITE; PS000187; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.3%; Score 88; DB 1; 67.7%; Pred. No. 0.0093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 SVSEIQFMHNLGKHLSSMERVEWLRKKLQDV 62
                                                                                         115 AA
                                                                        1 AVSEIGGGGGGGGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U15662; AAA82584.1; -; mRNA. PIR; JC4202; JC4202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                              Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
TISSUE=Parathyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P01268; 1ZWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                         Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                             CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                Name=PTH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       removed.
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                                                                                                                                             PTHY CANFA
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 AA; 12852 MW; 9FE8BCDE614BAC16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parathyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 84; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.028;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct protein sequencing; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR003625; Pthyrhorm_sub.
PANTHRE; PTR1810541; Pthyrhorm_sub;
Pfam; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       Pthyrhorm_sub; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                       EMBL; X05722; CAA29193.1; -; mRNA.
PIR; B26806; PTPG.
                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD010687; Pthyrhorm_sub;
SMART; SM00087; PTH; 1.
PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                         HSSP; P01270; 1BWX
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ID _PTHY_FELCA
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PTHY\_PIG RESULT 7

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Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Euarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Schmelzer H.J., Gross G., Mayer H.;
"Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  salts in
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STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
MEDINE=56079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
Nutley M.T., Parimi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger ribonucleic acid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
HEINTICH G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
Heinrich G., Kronenberg H.M., Sequence of the modeling parathyroid hormone. Nucleotide sequence of the hormone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87316938; PubMed=3628009; Schmelzer H.-J., Gross G., Widera G., Mayer H..; Wucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat."; Nucleic Acids Res. 15:6740-6740(1987).
                                                                                                                                                                                                                                                                              105 AA; 11684 MW; 18EF71B3F1CF5F70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1986 (Rél. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
Endocrinology 136:5600-5607(1995).

EMEL: $80127; AAP32220.1; -; mRNA.

HSSP: p01270: 1ZWB.

GO; GO:0005176; C:extracellular region; IEA.

GO; GO:0005179; F:hormone actrivity: IEA.

InterPro: IPR001415; Parathyrd.hrm.

InterPro: IPR003625; Phythorm sub.

Pfam; PF01279; Parathyroid; 1.

ProDom; PR010641; Pthythorm sub; 1.

ProDom; PR010697; PTH; 1.

ProDom; PR0010697; PTH; 1.

ProDom; PR0010697; PTH; 1.

ProCom; PR0010697; PTH; 1.

ProCom; PR0010697; PTH; 1.

ProCom; PR0010697; PTH; 1.

PROSITE; EN00135; PTH; 1.

PROSITE; EN00135; PTH; 1.
                                                                                                                                                                                                                                                                                                                                                      47.5%; Score 77; DB 2;
61.3%; Pred. No. 0.17;
live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 AVSEIQLMHNLGKHLASVERMQWLRKKLQDV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 AA
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.3%;
Marches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
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ID PTHY_RAT S1

AC PO4089; Q63473;

DT 01-NOV-1986 (Rel.

DT 10-NAY-2005 (Rel.

DT 10-NAY-2005 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hormone.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

"Molecular Cloning of feline preproparathyroid hormone.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion (By similarity).

-!- SUBCELLULAR LOCATION: Secreted (By similarity).

-!- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                             Felis silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley;
MEDILINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
Nutley M.T., Parimi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger ribonucleic acid.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Score 81; DB 1; Length 115; 61.3%; Pred. No. 0.063; Live 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
By similarity.
Parathyroid hormone.
80cD557cC6A1A47E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INCEPTO: 1PRO0145; Parathyrd hrm.
INCEPTO: IPRO01465; Pchyrhorm sub.
PANTHER: PTHR10541; Pchyrhorm sub.
PANTHER: PTHR10541; Pchyrhorm sub; 1.
PRAMTHER: PRSF001832; PTH; 1.
PRODOM; PD010687; Pthyrhorm_sub; 1.
SMART; SM00087; PTH; 1.
SMART; SM00087; PTH; 1.
HORMONE; Signal.
25 By Similar:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF309967; AAG30545.1; -; mRNA.
HSSP; P01268; 1ZWC.
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26 31 By
32 115 Pe
115 AA; 12921 MW;
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Matches 19, Conservative
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                                                                                                                                                                                                                   Felinae, Felis.
NCBI TaxID=9685;
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SEQUENCE
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32
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SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.; "Cloning of the murine gene encoding parathyroid hormone: genomic organization and nucleotide sequence."; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Thyroid;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                        Score 77; DB 1; Length 115;
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                           C -> Y (in Ref. 3).
A -> T (in Ref. 3).
A -> I (in Ref. 3).
V -> G (in Ref. 3).
7B434CFCA528B230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
11-MAY-1999 (TrEMBLrel. 10, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Parathyroid hormone precursor.
                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                     ENSRNOG00000014318; Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
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                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.19
3; Mismatches
                                                                     EMBL; K01268; AAA41979.1; -; Genomic_DNA.
EMBL; X05721; CAA29192.1; -; mRNA.
EMBL; M54875; AAA57156.1; -; mRNA.
                                                                                                     EMBL; S80127; -; NOT ANNOTATED_CDS; mRNA.
PIR; A05091; A05091.
                                                                                                                                                                                                                                                                                                Parathyroid
                                                                                                                                              RGJ; 3440; Pth.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR003626; PTH related.
InterPro; IPR003625; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; I.
PIRSF; PIRSF001832; PTH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                        ProDom; PD013225; PTH related; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
                                                                                                                                                                                                                                             SMART; SM00087; PTH; Î.
PROSITE; PS00335; PARATHYROID; 1.
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31
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18 C
23 A
33 V
62 V
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Best Local Similarity 61.3%;
Matches 19; Conservative
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Q9Z0L6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                32
18
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33
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115 AA;
                                                                                                                           HSSP; P01270; 1ZWB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                 Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Pth;
                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                     Ensemb1;
                                                   removed.
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S. Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; and mouse Cona sequences "." and mouse Cona sequences "." and mouse Cona sequences "."
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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P53349; Q60831; Q9R0U3; Q9R256;
D-007CT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Mitogen-activoted protein kinase kinase kinase 1 (EC 2.7.1.37)
(MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1).
Name=Map3k1; Synonyms=Mekk, Mekk1;
Mus musculus (Mouse).
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Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AF066075; AAC99656.1; -; Genomic_DNA.
EMBL; BC099456.1; -; mRNA.
HSSP; P01270; 12WB.
EMBEMBL; ENSMUSG0000059077; Wus musculus.
MGI; MGI:97709; Pth.
GO; GO:0005179; Pth.
GO; GO:0005179; Pthormone activity; IDA.
GO; GO:0005179; P:catracellular space; IDA.
GO; GO:0005179; P:chormone activity; IDA.
InterPro; IPR001415; Parathyrd_hrm.
InterPro; IPR001425; Pthythorm_sub;
PANTHER; PTHR10541; Pchythorm_sub;
PRNF; PIRSF001832; PTH; 1.
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parathyroid hormone.
DA43FABBCB4E2FD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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Local Similarity 58.1%; Pred. No. 0.33
les 18; Conservative 4; Mismatches
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TISSUE=Spleen;
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GO; GO: 0030334; P:regulation of cell migration; IMP.

GO; GO: 000179; P:transforming growth factor beta receptor si. . .; IMP.

GO; GO: 0042060; P:wound healing; IMP.

R InterPro; IPR00079; Prot kinase.

DR InterPro; IPR00329; Ser thr pkinase.

EnterPro; IPR003290; Ser thr pkinase.

EnterPro; IPR003903; UIM.

EnterPro; IPR003903; UIM.

EnterPro; IPR001341; Smf ENING.

ENGITE; PS00101; PR07EIN. KINASE ENING.

ENGOSITE; PS00104; ENING.

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T-SE LOSS of kinase activity and autophosphorylation.

T-SE LOSS of kinase activity and autophosphorylation.

T-A: Loss of kinase activity and autophosphorylation. Fails to activate MAP2K1, MAP2K4, MAP2K7, CHUK and IKBKB.

T-SE LOSS of kinase activity and autophosphorylation. Fails to activate autophosphorylation.

T-SE LOSS of kinase activity and autophosphorylation.

T-SE LOSS of kinase activity and autophosphorylation.

T-SE LOSS of MP-kappa-B transcription factor activity and reduced ability to activate MAP2K1, MAP2K7, No effect on AP-1 activity or activation of CCHUK and IKBKB. Loss of binding to IKBKB.

F-SA: LOSS of AP-1 and NP-kappa-B transcription factor activity. Reduced ability to activate MAP2K1, MAP2K4, MAP2K4, CHUK and IKBKB.

M-SA: LOSS of AP-1 and NP-kappa-B transcription factor activity. Reduced ability to activate MAP2K1, MAP2K4, MAP2K7, CHUK and IKBKB.

W-SA: LOSS of AP-1 and NP-kappa-B transcription factor activity. Reduced ability to activate MAP2K1, MAP2K4, MAP2K7, CHUK and IKBKB.

M-SA: LOSS of AP-1 and NP-kappa-B transcription factor activity. Reduced ability to activate MAP2K1, MAP2K4, MAP2K7, CHUK and IKBKB.

M-SA: LOSS of AP-1 and NP-kappa-B transcription factor activity. Reduced ability to activate MAP2K1, MAP2K4, MAP2K7, CHUK and IKBKB.

L-SA: LOSS of AP-1 tand NP-kappa-B transcription factor activity. Reduced ability to activate MAP2K1, MAP2K4, MAP2K7, CHUK and IKBKB.
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MAPZK7. Loss of binding to MAPZK4.
R-AR. Loss of AP-1 transcription factor activity, no effect on NF-Kappa-B
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ATP (By similarity).
Phosphothreonine.
Phosphothreonine.
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Pro-rich.
Pro-rich.
Poly-Ser.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTECT; F03489; --
EDBEGMED1; ENSWUSGG0000021754; Mus musculus.
MGT: MGT:1346872; Mmg3k1.
GO; GO:0001747; P:eye morphogenesis (sensu Mammalia); IMP.
GO; GO:0030389; P:posttive regulation of actin filament polym. . .; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           088351:IADAD, NDEXp=1; INTACt=EBI-447913, EBI-447960; P47809:Nap2k4; NDExp=1; IntAct=EBI-447913, EBI-447934; Q9QZH6:Stitpec; NDEXp=1; IntAct=EBI-447913, EBI-527020; INTACT=EBI-447913, EBI-527020; TISSUE SPECIFICTIY: Highly expressed in the heart and spleen while a lower level expression is seen in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thr-1393.
-!- SUBNITT: Binds both upstream activators and downstream substrates in multimolecular complexes through its N-terminus.
-!- INPERACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [6]
MUTION, INTERACTIONS WITH IKEKE AND MAP2K4, ENZYME REGULATION, AND MUTAGENESIS OF THR-1381; THR-1383; ISO-1384; PHE-1396; MET-1397; VAL-1401; LEU-1402; ARG-1403 AND GLY-1404.
Pubmed=14500727; DOI=10.1074/jbc.M304234200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tu Z., Lee F.S.;
Subdomain VIII is a specificity-determining region in MEKK1.";
J. Subdomain VIII is a specificity-determining region in MEKK1.";
J. Subdomain VIII is a specificity-determining region in MEKK1.";
J. Subdomain VIII is a specificity-determining region in MEKK1.";
J. Subdomain VIII is a specificity-determining region in MEKK1.";
Cascade. Activates the ERK and MAPZK1 and MAPZK4. Activates CHUK and IKBKB, the central protein kinases of the NF kappa-B pathway.
-!- CATALTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- CATALTIC MINITY.
-!- CATALTIC MI
                          MEDLINE=99455010, PubMed=10523642;
LO M., Yobhioka K., Akechi M., Yamashita S., Takamatsu N.,
Sugiyama K., Hibi M., Makabepu Y., Shiba T., Yamamoto K.-I.;
"JSAPI, a novel jun N-terminal protein kinase (JNK) binding protein
that functions as a scaffold factor in the JNK signaling pathway.";
Mol. Cell. Biol. 19:759-7548(1999).
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-!- FTM: Autophosphorylated.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MAP-kinase kinase kinase subfamily.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 SWIM-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson G.L., ^{\prime} A divergence in the MAP kinase regulatory network defined by MEK kinase and Raf.",
                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/C; TISSUE=Brain;
MEDLINE=93227040; PubMed=8385802;
Lange-Carter C.A., Pleiman C.M., Gardner A.M., Blumer K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [5]
ENZYME REGULATION, AND MUTAGENESIS OF THR-1381 AND THR-1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deak J.C., Templeton D.J., "Regulation of the activity of MEK kinase 1 (MEKK1) by autophosphorylation within the kinase activation domain."; Biochem. J. 322:185-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [4]
NUCLEOTIDE SEQUENCE OF 796-1493.
STRAIN=BALB/C; TISSUB=Heart;
Whitmarsh A.J., Shore P., Sharrocks A.D., Davis R.J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF117340; AAD25049-1; -; MRNA.
EMBL; AB014614; BAA65878.1; -; MRNA.
EMBL; L13103; AAA97500.1; ALT INIT; MRNA.
EMSL; US3470; AAA85038.1; -; MENA.
HSSP; Q16539; IKV1.
INTACt; PS3349; -.
                                                                                                                                                                                                                                                                  [3]
NUCLEOTIDE SEQUENCE OF 660-1493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 260:315-319(1993).
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Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R GO; GO: 0005524; F:ATP binding; IEA.

R GO; GO: 0005524; F:ATP binding; IEA.

R GO; GO: 0005524; F:ATP binding; IEA.

R GO; GO: 0005524; F:ATP binding; IEA.

R GO; GO: 0006501; F:kinae activity; IEA.

R GO; GO: 0006487; F:receptor activity; IEA.

R GO; GO: 0000155; F:two-component response regulator activity; IEA.

R GO; GO: 0000155; F:two-component seponse regulator activity; IEA.

R GO; GO: 0000155; F:two-component seponse regulator activity; IEA.

R GO; GO: 0000156; F:two-component signal transduction system (p. . .; IEA.)

R GO; GO: 0000160; P:two-component signal transduction system (p. . .; IEA.)

R GO; GO: 0000160; P:two-component signal transduction system (p. . .; IEA.)

R InterPro; IPR003048; GAF.

R InterPro; IPR003048; Response_reg.

R Fam; PF001590; GAF: 1.

R Fam; PF00152; H:ASKA; I.

R Fam; PF00152; H:ASKA; I.

R R PROMOM: PF0000039; Response_reg; 1.
                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2005 (TrEMBLrel. 27, Last sequence update)
05-JUL-2006 (TrEMBLrel. 29, Last annotation update)
Putative ethylene receptor-like protein 2.

Name=P0474F11.19-1; Synonyms=OJ1119_A01.4-1;
Oryza sativa (isponica cultivar-group).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            G-5A: Loss of AP-1 and NF-kappa-B transcription factor activity.
GGGALGGSGA -> ALGGSG (in Ref. 2).
Wissing (in Ref. 2).
W -> E (in Ref. 2).
S -> C (in Ref. 2).
V -> A (in Ref. 2).
V -> L (in Ref. 3).
V -> L (in Ref. 3).
V -> L (in Ref. 3).
                                                                                                                                                                                                                               10; Indels 19;
                                                                                                                                                                                                                                                             -----SMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                          20 ASPEAGGGGGGGGALQGSGAPAAGAAGLLREPGSAGRERADWRRRQLRKV 69
                                                                                                                                                                                              Score 73.5; DB 1; Length 1493;
Pred. No. 6.8;
4; Mismatches 10; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki T., Margumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, clone:OJ1119 AO1."; Submitted (AŪG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  CA65C9B7703C6BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki T., Marsumoto T., Yamamoto K.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                        770 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AP004878; BAD23111.1; -; Genomic_DNA. BMBL, AP004020; BAD22879.1; -; Genomic_DNA. Gramene; Q6K708; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00065; GAF; 1.
SMART; SM00388; HisKA; 1.
SMART; SM00448; REC; 1.
PROSITE; PS50109; HIS KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
   activity
                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                             1 AVSEIGGGGGGGGLN-----
                                                                                                                                                                                                                 34.0%;
                                                                                                                                                                                                    45.48;
                                                                                                                                                                    AA; 161289
                                                                                                                                                                                                                                                                                                                                                                     QEK708 ORYSA PRELIMINARY;
QEK708;
                                                                                                                                                                                                                                  17; Conservative
                                                           103
257
307
413
559
883
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=39947;
                                                                                                                         559
883
1467
1493
                                                            CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                            CONFLICT
                 MUTAGEN
                                                                                                                                                                                                                                                                                                                                                            ORYSA
                                                                                                                                                                                                                                                                                                                                          Matches
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DR GO; GO: 0016020; C:membrane; IEA.

DR GO; GO: 0016020; C:membrane; IEA.

DR GO; GO: 0016020; C:membrane; IEA.

CO; GO: 0016320; F:ATP binding; IEA.

CO; GO: 0016301; F:kinase activity; IEA.

CO; GO: 0016301; F:kinase activity; IEA.

CO; GO: 0000155; F:two-component response regulator activity; IEA.

CO; GO: 0000155; F:two-component response regulator activity; IEA.

CO; GO: 0000155; F:two-component signal transduction; IEA.

CO; GO: 0000160; F:two-component signal transduction system (p. . .; IEA.)

CO; GO: 0000160; F:two-component signal transduction system (p. . .; IEA.)

CO; GO: 0000160; F:two-component signal transduction system (p. . .; IEA.)

CO; GO: 0000189; ArPbind_ATPase.

InterPro; IPR005467; His kinase.

InterPro; IPR005467; His kinase.

InterPro; IPR00189; Response_reg.

Refam; PP01850; GAF; II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                       ٠<u>.</u>
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in rice during development, and in response to indole-1-acetic acid and silver ions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pubbled=14754915; DOI=10.1093/jxb/erh055; Yau C.P., Wang L., Yu M., Zee S.Y., Yip W.K.; "Differential expression of three genes encoding an ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 836;
                                                         DB 2; Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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770 AA; 84998 MW; E4F7151DB57B973B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                        836 AA
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Pred. No. 8.5;
                                                         Score 70.5; Di
Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0109; HIS_KIN; 1.
PROSITE; PSS0110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 GGGGGGGGLWSMDSIFRW--QKVSDL 136
                                                                                                                                                                                                                       46 GGGGGGGGLWSMDSIFRW--QKVSDL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGGGGGLNSMERV-EWLRKKLQDV 31
                                                                                                                                                                                    6 GGGGGGGGLNSMERV-EWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (indica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. EXP. BOL. 55:547-556(2004).
EMBL; AY434735; AAR08915.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02518; HATPase_c; 1.
Pfam; PF00512; HisKA; 1.
Pfam; PF00072; Response_reg; 1.
ProDom; PD000039; Response_reg; 1.
                                                         43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative ethylene receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00065; GAF; 1.
SMART; SM00388; HisKA; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  QETSK2 ORYSA PRELIMINARY;
QETSK2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 55.6 es 15; Conservative
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                             Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=ETR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                        RESULT 14

QGTSK2_ORYSA_
DC QGTSK2_OR

AC QGTSK2_OR

DT QS-JUL-20

DT OS-JUL-20

DT OS-JUL-20

DT OS-JUL-20

DT OS-JUL-20

DE PLIALITY

OS ORYSA BARA

OS ORYSA BARA

OS ORYSA BARA

OS ORYSA BARA

NUCLECTII

RX PLUMGC=17

RY PLUMG=17

RY PLUMGC=17

RY PLU
                                                                Query Match
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094401 ORYSA PRELIMINARY; PRT; 836 AA.

Dr 094401 ORYSA PRELIMINARY; PRT; 836 AA.

Dr 01-007-2001 (TREBBLEA. 22, Last sequence update)

Dr 01-007-2001 (TREBBLEA. 22, Last sequence update)

Dr 01-007-2002 (TREBBLEA. 22, Last sequence update)

Dr 01-WAR. 2004 (TREBBLEA. 22, Last sequence update)

Dr 01-WAR. 2004 (TREBBLEA. 22, Last sequence update)

Core Skravyce receptor-like procein 2.

OC Shravicodese; Oryzae. Oryzae.

OC Sparmacophyca; Magnoliophyca; Liliopsida; Poales; Poaceae;

Core Brinaricodese; Oryzae. Oryzae.

OC Sparmacophyca; Magnoliophyca; Liliopsida; Poales; Poaceae;

NRI TAXACCENTIDE SEQUENCE.

RR NUCLEOTIDE SEQUENCE.

RR NUCLEOTION SEQUENCE.

RR NUCLEOTIDE SEQUENCE.

RR SCOOLOSSORY Fraceoponent sensor molecule activity; IEA.

RC OCOOLOSSORY Fraceoponent sensor molecule activity; IEA.

RC OCOOLOSSORY Fraceoponent sensor molecule sequence.

RR SCOOLOSSORY RESEQUENCE.

RR SCOOLOSSORY RESEQ
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Search completed: November 21, 2005, 16:15:13 Job time : 148.5 secs

112 GGGGGGGLWSMDSIFRW--QKVSDL 136

g

Appli Appli Appli Appli Appli Appli Appli Appli Appli

sequence 271, sequence 271, sequence 1, sequence 1, sequence 1, sequence 1, sequence 1, sequence 1, sequence 6, sequence 1, sequence 1, sequence 1, sequence 1, sequence 1, sequence 2, sequence 2, sequence 2, sequence 1, sequence 2, sequence 1, sequence 1, sequence 2, sequence 1, sequence 2, sequence 1, sequence 2, sequence 2, sequence 2, sequence 1, se

165, 271, 271, 9, Ap

Sequence Sequence Sequence

```
Sequence 29, Application PC/TUS9515800
GENERAL INFORMATION:
APPLICANT: BIONEDIASKA, Inc.
TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING
TITLE OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRICTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STRRET: 3100 Norwest Center, 90 S. 7th Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 38;
US-09-536-785A-32
US-09-843-221A-165
US-09-643-221A-165
US-09-657-276-271
US-09-467-276-271
US-09-467-276-271
US-08-033-099-1
US-08-2495C-1
US-08-443-863-1
US-08-443-09-1
US-08-443-09-1
US-08-443-09-1
US-08-443-00-1
US-08-449-500-1
US-08-449-500-1
US-08-449-500-1
US-08-449-317A-1
US-08-449-317A-1
US-08-449-317A-1
US-08-449-317A-1
US-08-449-317A-1
US-08-447-622-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100; DB 4;
Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: PCT/US95/15800
07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICALL...
FILING DATE: 07-DEC-12...
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,530
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: CARTER, Charles G
REGISTRATION NUMBER: 35,093
REFRENCE/DOCKET NUMBER: 8648.4
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Minneapolis
STATE: MN
COUNTRY: U.S.A.
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASEEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/156
APPLICATION NUMBER: PCT/US95/156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.7%;
74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internal
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO FRAGMENT TYPE: i ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                      RESULT 1
PCT-US95-15800-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-15800-29
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                                                                                                     November 21, 2005, 16:05:03; Search time 33 Seconds (without alignments) 77.665 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14,
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Sequence 1
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-08-142-5518-37
US-08-142-5518-46
US-08-142-5518-56
US-08-142-5518-56
US-09-147-800-5
US-09-147-800-5
US-09-147-800-5
US-09-147-800-5
US-09-143-221A-12
US-09-843-221A-162
US-09-843-221A-163
US-09-843-221A-163
US-09-843-221A-163
US-09-843-221A-163
US-09-843-221A-163
US-09-144-556A-8
US-08-691-647C-6
US-08-691-647C-6
US-08-904-760B-6
US-08-904-760B-6
US-08-904-760B-14
                                                                                                                                                                                         1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
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                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                  572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                  Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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162
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Match Length DB
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Score

Regult

Post-processing:

Database :

Minimum DB 8 Maximum DB 8

Scoring table:

Perfect score:

Sequence:

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/note= "Where "Xaa" is selected from the group consisting of Hol, Ho, a homoserine amide, or the sequence of amino acids comprising residues 35-84 of PTH."
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Sequence 37, Application US/08142551B
Sequence 37, Application US/08142551B
CENDEAL INFORMATION:
APPLICANT: S8146A
APPLICANT: S1046A
APPLICANT: SALICK, HARDIG E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES:
ADDRESSEE: BUTTS, DOANE, Swecker & Mathis
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUTTS, DOANE, Swecker & Mathis
STREET: Virginia
COUNTRY: Virginia
COUNTRY: Alexandria
SIATE: Virginia
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: US/08/142,551B
FILING BATE: 25-OCT-1993
CCLASSIFICATION NUMBER: US 08/077,296
FILING DATE: 12-UN-1993
PRIOR APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1993
PRIOR APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UN-1992
PRIOR APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGRATING DATE:
DEFINICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGRATING DATE:
DEFINICATION NUMBER: US 07/965,677
FILING DATE: SALICATION DATE:
DEFINICATION NUMBER: US 07/965,677
FILING DATE: DEFINICATION DATE:
DEFINICATION NUMBER: US 07/965,677
PULLING DATE: DEFINICATION DATE:
DEFINICATION NUMBER: US 07/965,677
PULLING DATE: DEFINICATION DATE:
DEFINICATION DATE: DEFINICATION DATE:
DEFINICATION NUMBER: US 07/965,677
PULLING DATE: DEFINICATION DATE:
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REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEPAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Oldenburg, Kevin R. APPLICANT: Selick, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
COATION: 35
COTHER INFORMATION: from the
COTHER INFORMATION: from the
COTHER INFORMATION: amide,
COTHER INFORMATION: residue,
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LOCATION: 35
LOCATION: 35
OCHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
OCHER INFORMATION: amide, or the sequence of amino acids comprising
OTHER INFORMATION: residues 35-84 of PTH..
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         Gaps
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APPLICANT: Selick, Harold B.
APPLICANT: Selick, Harold B.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 13.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
GITY: Abandria
GITY: Virginia
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         Indels
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COUNTRY:
COUNTRY:
COUNTRY:
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
COMPUTER:
COMP
         7;
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                                                                                  1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
                                                                                                                                          1 SVSEIGLMHNLGKHLNSMERVEWLRKKLQDV 31
         1; Mismatches
                                                                                                                                                                                                                                                                                    RESULT 2
US-08-142-551B-34
Sequence 34, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acids
TOPOLOGY: unknown
         23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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: US
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         Matches
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ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site
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    Virginia
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Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
      COMPOUNDS WITH PTH ACTIVITY AND RECOMBINANT DNA VECTORS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.5%; Score 98; DB 1; Length 35; Best Local Similarity 71.0%; Pred. No. 2.8e-05; Matches 22; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                        CCUMPTRY: US
ZIP: 22313
COMPUTER E2313
COMPUTER PADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 25-OCT-1993
CLASSIFICATION NUMBER: US 08/077,296
FILING DATE: 12-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
PRIOR APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGRNT INPORMATION:
REFERENCY/OCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPONE: (415) 854-740
TELEFRAICH CHARACTERISTICS:
LENOTH: 35 amino acide
"WUDE: Amino acide
"WUDE: Amino acide
"WUDE: Amino acide
"WUDE: Amino acide
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVIT TITLE OF INVENTION: RECOMBINANT DNA VECTORS EN NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS: ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
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OTHER INFORMATION: 0
OTHER INFORMATION: 6
OTHER INFORMATION: x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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US-08-142-551B-40
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LOCATION: 35
CTHER INFORMATION: /note= "Where "Xaa" is selected
CTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
CTHER INFORMATION: amide, or the sequence of amino acids comprising
CTHER INFORMATION: residues 35-84 of PTH."
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US-08-142-51B-52
Sequence 52, Application US/08142551B
Sequence 52, Application US/08142551B
Sequence 52, Application US/08142551B
Setent No. 5814603
GENERAL INFORMATION:
Oldenburg, Kevin R.
APPLICANT: Solick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 35;
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Query Match
59.3%; Score 96; DB 1; Le
Best Local Similarity 71.0%; Pred. No. 4.9e-05;
Matches 22; Conservative 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria STATE: Virginia COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                 NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMUNICATION INFORMATION:
TELEPAN: (415) 854-7400
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
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/note= "Where "Xaa" is selected
from the group consisting of Hol, Ho, a homoserine
amide, or the sequence of amino acids comprising
residues 35-84 of PTH."
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| Sequence 6, Application US/09447800
| Patent No. 6537965
| GENERAL INPORMATION:
| APPLICANT: BRINGHREST, F. RICHARD
| APPLICANT: TAKASU, HISASHI
| APPLICANT: GARDELLA, THOMAS J.
| TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
| TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
| TITLE OF INVENTION: ANALOGS
| TITL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.3%; Score 96; DB 1; Length 35; 71.0%; Pred. No. 4.9e-05; tive 2; Mismatches 7; Indels
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FILING DATE: 14-JUN-1993

RIOR APPLICATION DATE: 30 07/898,219

PELING DATE: 12-JUN-192

READRA PELICATION DATE: 12-JUN-192

READRA PELICATION DATE: 20-JUN-1992

ATTORNEY/AGENT INFORMATION: NAME: SA'188, Gerald F. NAME: SA'189, Gerald F. NEGISTATION NUMBER: 30,113

REFERENCE/DOCKET NUMBER: 000324-010

TELEPHONE: (415) 84-7400

TELEPHONE: (415) 84-8275

INFORMATION FOR ESO ID NO: 56: SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids

TYPE: mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Desamino Ala
US-09-447-800-6
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LOCATION: 35
OTHER INFORMATION: from ti
OTHER INFORMATION: mide,
OTHER INFORMATION: mide,
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Best Local Similarity 71.0<sup>3</sup>
Matches 22; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-142-551B-56
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OTHER INPORMATION: from the group consisting of Hol, Ho, a homoserine of THER INFORMATION: amide, or the sequence of amino acids comprising of Hol. "OTHER INFORMATION: residues 35-84 of PTH."
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Sequence 56, Application US/08142551B
Sequence 56, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEB: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CONTY: Alexandria
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59.3%; Score 96; DB 1; Length 35;
Best Local Similarity 71.0%; Pred. No. 4.9e-05;
Matches 22; Conservative 2; Mismatches 7; Indels
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CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
                     PatentIn Release #1.0, Version #1.25
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                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA: US 08/077,296
FILING DATE: 12-JUN-1993
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAIS, GET-ald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Virginia
COUNTRY: US
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
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                                                                                                  GENERAL INFORMATION:
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKASU, HISASHI
APPLICANT: GARDELLA, THOMAS J.
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMALOGS
TITLE OF INVENTION: AMALOGS
FILE REFERENCE: 0609,4630001
CURRENT APPLICATION NUMBER: US/09/447,800
CURRENT FILING DATE: 1999-11-23
EARLIER PAPLICATION NUMBER: 60/110,152
EARLIER PILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE PATENTION OF: 2.1
SEQ ID NO 5
LENGTH: 34
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APPLICANT: NAKAGAWA, Shizue
APPLICANT: HABASHITA, Junko
APPLICANT: TAKETOMI, Shigehisa
APPLICANT: TAKETOMI, Shigehisa
TITLB OF INVENITION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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                                                                Sequence 5, Application US/09447800 Patent No. 6537965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALLOWARD CONLIN, David G
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 465
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES
LOCATION: (1)
CTHER INFORMATION: Desamino Ala
US-09-447-800-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617)523-6440
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CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-09-044-536A-12
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                                                US-09-447-800-5
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GENERAL INFORMATION:
APPLICANT: KOSTEMUIK, PAUL
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: RELATED PROTEIN
FILE REFERENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT APPLICATION NUMBER: G0/266,673
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATENTIN VEFSION 3:1
SEQ ID NOS: 170
SEC ID NOS
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APPLICANT: KOSTENUIK, PAUL
APPLICANT: LIU, CHONN-FA
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID ITTLE OF INVENTION: RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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58.0%; Score 94; DB 2; Length 34;
Best Local Similarity 71.0%; Pred. No. 8.3e-05;
Matches 22; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 11

OTHER INFORMATION: /product= "Xaa=Ala(2-Naph)"
US-09-044-536A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 58.0%; Score 94; DB 2; Le
Best Local Similarity 71.0%; Pred. No. 8.3e-05;
Matches 22; Conservative 1; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Patent No. 6756480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09843221A
Patent No. 6756480
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   NAME/KEY: partial peptide LOCATION: 1..34
                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: Modified-site
         STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
amino acid
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GENERAL INFORMATION:
APPLICANT: KOSTENILY PAUL
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIACEY, DAVID LEE
APPLICANT: LIACEY, DAVID LEE
TITLE OF INVENTION: RELATED PROTEIN
FILE REFREENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
FILE REPREENCE: A-665B
CURRENT APPLICATION NUMBER: 60/266,673
PRIOR APPLICATION NUMBER: 60/214,860
PRIOR APPLICATION NUMBER: 60/214,860
PRIOR APPLICATION NUMBER: 60/200,053
PRIOR APPLICATION NUMBER: 60/200,053
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.1
LENGTH: 34
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CTHER INFORMATION: Preferred embodiments - PTH
NAME/KES:
NAME/KES:
LOCATION: (34)...(34)
COTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163
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| Sequence 43, Application US/08142551B |
| Patent No. 5814603 |
| Canbral InvoRwATION |
| APPLICANT: Oldenburg, Kevin R. APPLICANT: Oldenburg, Kevin R. APPLICANT: Oldenburg, Marold B. TITLE OF INVENTION COMPOUNDS WITH PTH ACTIVITY AND TITLE OF INVENTION COMPOUNDS WITH PTH ACTIVITY AND TITLE OF INVENTION RECOMBINANT DNA VECTORS ENCODING SAME CORRESPONDERS: 132 |
| CORRESPONDERS: 132 |
| CORRESPONDERS: ADDRESS: CORRESPONDERS: BUTCH ACTIVITY AND TITLE OF INVENTION COMPOUNDS AND CORRESPONDERS: BUTCH ACTIVITY AND TITLE OF INVENTION CORRESPONDERS: 30 |
| CORRESPONDERS: 30 |
| CORRESPONDERS: ADDRESS: CORRESPONDERS: ADDRESS: ADDRESS
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ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
STARET: 1099 Prince Street
COUNTRY: Ustains
COUNTRY: Ustains
COMPUTER: Virginia
COMPUTER: Packer
COMPUTER: TRADABLE FORM:
MEDIUM TYPE: FLORM:
FCOMPUTER: TRADABLE FORM:
MEDIUM TYPE: FLORM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 12-00N-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 11-00N-1993
PRIOR APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-00N-1993
PRIOR APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-00N-1993
PRIOR APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-00N-1993
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-00N-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVSEIQLMHNKGKHINSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
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US-09-043-21A-162
US-09-043-21A-162
Sequence 162, Application US/09843221A
Sequence 162, Application US/09843221A
Sequence 162, Application US/09843221A
Sequence 16756480
Sequence 1675680
Sequence 167580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAWE/KEY: misc_feature
; LOCATION: (34)...(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.0%; Score 94; DB 2; Length 34; Best Local Similarity 71.0%; Pred. No. 8.3e-05; Matches 22; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.0%; Score 94; DB 2; Length 34; Best Local Similarity 71.0%; Pred. No. 8.3e-05; Matches 22; Conservative 1; Mismatches 8; Indels
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           FILE REFERENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT TILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 34
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 163, Application US/09843221A Patent No. 6756480
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ORGANISM: Artificial Sequence
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US-09-843-221A-163
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NAME: Swiss, Gerald F.

REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMUNICATION INCOMATION:
TELEPHONE: (415) 854-7400
TELEPRAX: (415) 854-8275
INPORMATION FOR EXQ ID No: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 anino acids
TYPE: amino acids
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEX: Modified-site
COATION: 35
OTHER INFORMATION: /note= "where "Xaa" is selected
OTHER INFORMATION: amide, or the group consisting of Hol, Ho, a homoserine
OTHER INFORMATION: residues 35-84 of PTH:"
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Best Local Similarity 71.0%; Pred. No. 8.6e-05;
Matches 22; Conservative 2; Mismatches 7; Indels
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Search completed: November 21, 2005, 16:16:22 Job time : 34 secs

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20, Appl
17, Appl
18, Appl
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Sequence 19, Appl
                                                                     (without alignments)
117.219 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163,
                                                           November 21, 2005, 16:15:23 ; Search time 110.5 Seconds
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Sequence 1
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                                                                                                                                                                                                                                                                                       Published Applications AA Main:*

(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-997-822-4
US-10-997-762-21
US-10-917-762-21
US-10-91-928-6
US-10-91-928-6
US-09-843-221A-17
US-09-843-221A-162
US-09-843-221A-163
US-09-999-608-18
US-09-999-608-18
US-09-999-608-163
US-09-999-608-163
US-10-899-608-163
US-10-899-037-18
US-10-899-037-162
US-10-899-037-163
US-10-892-025-22
US-10-892-025-22
US-10-892-025-22
US-10-892-025-22
US-10-892-025-22
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3-09-843-221A-165
3-09-999-608-27
                                                                                                               162
1 AVSEIGGGGGGGGLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-440-473-2
                                                                                                                                                                           1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                    US-09-475-158A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length
          Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                             Scoring table:
                                        OM protein
                                                                                                                          Sequence:
                                                                                                                                                                           Searched:
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                                                                                                    Title:
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US-10-99/-078-132
; Sequence 132, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Peng, L.
; APPLICANT: Restoragen, Inc.
; PILE REFERENCE: 1627.010US1
; FILE REFERENCE: 2004-11-24
; PRIOR PAPLICATION NUMBER: US/10/997,078
; PRIOR PELING DATE: 2003-05-24
; PRIOR PELING DATE: 2003-05-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 132
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                                                           Sequence 2, Appli
Sequence 20, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 21, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
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Sequence 16,
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Sequence
Sequence
Sequence
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Sequence
Sequence
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48 VGGGGGPRSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/10997762
Publication No. US20050227313A1
GENERAL INFORMATION:
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Polypeptide Cleavage Process
FILE REFERENCE: LS7.025013
CURRENT FILING DATE: 2004-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
64.2%; Score 104; DB 5; 1
Best Local Similarity 59.0%; Pred. No. 6.7e-05;
Matches 23; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GGGLNSMERVEWLRKKLQDV
US-10-839-037-27

US-10-839-037-165

US-11-066-697-21

US-11-040-557-2

US-11-040-557-2

US-11-040-557-20

US-11-040-557-20

US-11-040-557-21

US-11-040-557-21

US-11-040-557-21

US-11-040-557-21

US-11-040-557-21

US-09-169-786-3

US-09-928-0478-6

US-09-928-0478-6

US-09-928-0488-6

US-09-928-0488-6

US-09-928-0488-6
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       US-10-997-078-132
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US-10-997-762-19
      LENGTH: 89
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Sequence 6, Application US/10361928
; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GRRERAL INFORMATION:
APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISAGHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: ANALOGS
; TITLE OF INVENTION: ANALOGS
; TITLE OF INVENTION: ANALOGS
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT APPLICATION NUMBER: 09/447,800
; RIOR APPLICATION NUMBER: 09/447,800
; RIOR PILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 6
; SEQ ID NO 6
; LENGTH: 33
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Publication No. US20030144209A1
GENERAL INFORMATION:
APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKASU, HISASHI
TITLE OF INVENTION: AMALOGS
FILLE REFERENCE: 609,463000,946300,963000
CURRENT APPLICANT: LOS 46300,9463000
CURRENT FILING DATE: 2003-02-11
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0
                                                                                                                                                                                                                                                                                                          Length 141;
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                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88
                                                                                                                                                                                                                                                                                                                                                                                                          5 IGGGGGG------GGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                          Score 103; DB 5; Le
Pred. No. 0.00014;
1; Mismatches 3;
                                                                                                                                                                                                                                          , OTHER INFORMATION: A synthetic chimeric protein US-10-997-762-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
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PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 23
SOFTWARE FREISEQ FOR Windows Version 4.0
SEQ ID NO 21
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Desamino Ala
US-10-361-928-6
                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                            ch
l Similarity 56.1%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                                                                                                                     Query Match

Query Match

G3.6%; Score 103; DB 5; Length 91;

B4 56.1%; Pred. No. 9e-05;

Matches 23; Conservative 1; Mismatches 3; Indels
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48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLLQDV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GGGLNSMERVEWLRKKLODV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 VGGGGGPRCHSVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10997822
| Sequence 4, Application US/10997822
| Publication No. US20050227314A1
| GENERAL INFORMATION:
| APPLICANT: Holmquier, B.
| APPLICANT: SCTYON, N.
| APPLICANT: SCTYON, N.
| APPLICANT: SCTYON, N.
| APPLICANT: SCTYON, N.
| TILE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
| FILE REFRENCE: 1627, 0.01U61
| CURRENT APPLICATION NUMBER: US/10/997,822
| CURRENT FILING DATE: 2004-11-24
| PRIOR FILING DATE: 2003-05-23
| PRIOR FILING DATE: 2003-05-24
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: FastESQ for Windows Version 4.0
| SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/10997762
FUDLICALION NO. US20050227313A1
GENERAL INFORMATION:
APPLICANT: Sec. Jin Seog
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Polypeptide Cleavage Process
FILE REPREBENCE: 1627.026US1
CURRENT APPLICATION NUMBER: US/10/997,762
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16468
                                                                                                                                                                                           TYPE: PRT
ORGANIEM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A synthetic chimeric protein
US-10-997-762-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103; DB 5;
Pred. No. 9e-05;
1; Mismatches
  PRIOR APPLICATION NUMBER: PCT/USO3/16468
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FABLESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 56.1%;
Matches 23; Conservative
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US-10-997-762-21
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US-09-843-221A-18
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Sequence 20, Application US/10892025
Publication No. US20050065071A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Whitfield, James F
TITLE OF INVENTION: CYCLIC ANALOGS OF HUMAN PARATHYROID
TITLE OF INVENTION: HYPRENEUFERATIVE SKIN CELLS
FILE REFERENCE: 3583.1000-001
CURRENT APPLICATION NUMBER: US/10/892,025
CURRENT APPLICATION NUMBER: 05/407-15
PRIOR FILING DATE: 2003-07-15
PRIOR FILING DATE: 2003-07-15
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His-Asn-Phe-X; where X is OR or NHR; and R is
hydrogen or a linear or branched chain alkyl, acyl
or aryl group
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                                                                                                                                                                                                                                                                                                                                                              Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                            Query Match 58.6%; Score 95; DB 4; 1
Best Local Similarity 74.2%; Pred. No. 0.00032;
Matches 23; Conservative 0; Mismatches 8.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
SEQ ID NO 20
                PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/110,152
PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 34
APPLICATION NUMBER: 09/447,800
                                                                                                                                                                                                                                                                     LOCATION: (1) CTHER INFORMATION: Desamino Ala US-10-361-928-5
                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapien
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CTHER INFORMATION: Y
OTHER INFORMATION: H
CTHER INFORMATION: H
CTHER INFORMATION: US-10-892-025-20
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NAME/KEY: VARIANT
LOCATION: 8
OTHER INFORMATION: 1
OTHER INFORMATION: n
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OTHER INFORMATION:
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NAME/KEY: MOD_RES
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Sequence 18, Application US/09843221A
Publication No. US20030039654A1
Publication No. US20030039654A1
APPLICANT: NOSTENDIK, PAUL
APPLICANT: LIU, CHUAN FA
APPLICANT: LIU, CHUAN FA
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID #
TITLE OF INVENTION: RELATED PROTEIN
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58.0%; Score 94; DB 3; Length 34;
Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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CURRENT APPLICATION NUMBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/246,673
PRIOR APPLICATION NUMBER: 60/214,860
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER: OF SEQ ID NOS: 170
SEQ ID NO 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: modified human PTH
US-09-843-221A-17
Sequence 17, Application US/09843221A
Publication No. US20030039654A1
GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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US-09-999-608-17

US-09-999-608-17

US-09-999-608-17

Sequence 17, Application US/09999608

Publication No. US20050124537A1

GENERAL INFORMATION

PEDLICANT: GEGG, COLIN V.

APPLICANT: JARCSINSKI, MARK ANTHONY

APPLICANT: ALNSTLER, CLAF BORIS

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID

TITLE OF INVENTION: MODULATORS OF RECEPTORS

FILE REPERBACE: A-665C

CURRENT FILING DATE: 2002-03-11

PRIOR PELICATION NUMBER: US 60/266,673

PRIOR PELICATION NUMBER: US 60/266,673

PRIOR PELICATION NUMBER: US 60/214,860

PRIOR PELICATION NUMBER: US 60/214,860

PRIOR PELICATION NUMBER: US 60/214,860

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 193

SEQ ID NO 17

LENGTH: 34

TAVER: DATE

LENGTH: 34

TAVER: DATE
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| Sequence 18, Application US/09999608
| Publication No. US20050124537A1
| GENERAL INPORMATION:
| APPLICANT: KOSTENUIK, PAUL.
| APPLICANT: APPLICANT: MUSTERN, OLAF BORN:
| APPLICANT: APPLICANT: MUSTERN, OLAF BORN:
| TITLE OF INVENTION: MODULAPORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
| TITLE OF INVENTION: MODULAPORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
| TITLE OF INVENTION: MODULAPORS OF SECRET OR SECRET
; LOCATION: (34)...(34)
; OTHER INFORMATION: Optional linker and Pc domain attached at the C-terminus
US-09-643-221A-163
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                                                                                                                                                                                                                                                                                                                                                      1 AVSEIGGGGGGGGLNSMERVEWLRKKLODV 31
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ORGANISM: Artificial Sequence
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US-09-843-221A-162

US-09-843-221A-162

Sequence 162, Application US/09843221A

Publication No. US20030039654A1

SEQUENCE INTRORMATION:

APPLICANT: LIU, CHUAN-FA

APPLICANT: LIU, CHUAN-FA

TITLE OF INVENTION: RELATED PROTEIN

FILE REFERENCE: A-665B

CURRENT FILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: US/09/843,221A

CURRENT FILING DATE: 2001-02-06

PRIOR FILING DATE: 2000-06-28

SOFTWARKE: PARENTE NOWBER: 60/200,053

PRIOR FILING DATE: 2000-06-28

SOFTWARKE: PARENTE NOWBER: 90/200,053

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US-09-643-221A-163

US-09-643-221A-163

Sequence 163, Application US/09843221A

Publication No. US20030039654A1

Sequence 163, Application US/09843221A

SEQUENCE INFORMATION:
APPLICANT: LIU, CHUAN-FA

APPLICANT: LIU, CHUAN-FA

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE TITLE OF INVENTION: RELATED PROTEIN

TITLE OF INVENTION: RELATED PROTEIN

TITLE OF INVENTION: RELATED PROTEIN

TITLE OF INVENTION: RELATED PROTEIN

FILE REPRENCE 3-6656

PRIOR APPLICATION NUMBER: US/09/843,221A

CURRENT FILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/214,860

PRIOR APPLICATION NUMBER: 60/214,860

PRIOR APPLICATION NUMBER: 60/200,053

PRIOR APPLICATION NUMBER: 60/200,053

PRIOR FILING DATE: 2000-04-27

WARMADED OF GED IN NACE: 1700-04-27
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NAME/KEY: misc_feature
LOCATION: (34)-.(34)
OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.0%; Score 94; DB 3; Length 34; Best Local Similarity 71.0%; Pred. No. 0.00042; Matches 22; Conservative 1; Mismatches 8; Indels
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    SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVSEIQLMHNRGKHLNSMERVEWLRKKLQDV 31
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SOFTWARE: Patentin version 3.1
SEQ ID NO 163
LENGTH: 34
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ORGANISM: Artificial Sequence
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Search completed: November 21, 2005, 16:34:42 Job time : 110.5 secs
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APPLICANT: JAROSINSKI, MARK ANTHONY
APPLICANT: JAROSINSKI, MARK ENTHONY
APPLICANT: ALBUSTER, OLER BORIS
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

| LOCATION: 34)...(34)

| OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-09-999-608-162
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1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDV 31
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CURRENT APPLICATION NUMBER: US/09/99,608
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/843,221
PRIOR APPLICATION NUMBER: US 60/266,673
PRIOR FILING DATE: 2001-04-26
PRIOR FILING DATE: 2001-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 193
SOFTWARE: Patentin version 3.2
LENGTH: 34
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: US 60/200,053
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 193
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 34
                                                                                                                                                                                                                                                         ; OTHER INFORMATION: modified human PTH
US-09-999-608-18
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Publication No. US20050124537A1
GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 162, Application US/0999608
Publication No. US20050124537A1
GENERAL INFORMATION:
APPLICANT: KOSTENUIK, PAUL
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-999-608-162
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APPLICANT: JAROSINSKI, MARK ANTHONY
APPLICANT: JAROSINSKI, MARK ANTHONY
APPLICANT: KINSTLER, OLAF BORIS
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
TITLE OF INVENTION: HORMONE-RELATED PROTEIN
CURRENT APPLICATION NUMBER: US/09/999,608
CURRENT FILING DATE: 2001-03-11
PRIOR APPLICATION NUMBER: US 60/266,673
PRIOR APPLICATION NUMBER: US 60/214,860
PRIOR APPLICATION NUMBER: US 60/214,860
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 193
SOFTWARE: PARENT PARENT VERICALION VERSION 3.2
SEQ ID NOS: 193
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Best Local Similarity 71.0%; Pred. No. 0.00042;
Matches 22; Conservative 1; Mismatches 8;
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ORGANISM: Artificial Sequence
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TYPE: PRT
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Sequence 3, Appli
Sequence 21, Appli
Sequence 21, Appl
Sequence 64, Appli
Sequence 7, Appli
Sequence 32, Appli
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                                                              November 21, 2005, 16:16:29 ; Search time 4 Seconds
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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8: /cgn2_6/ptodata/2/pubpaa/US1I_NEW_PUB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-110-975-798-3
US-110-957-569-64
US-110-841-129-7
US-110-06-59-32
US-110-06-59-32
US-110-06-943-22
US-1110-65-943-24
US-110-65-943-24
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US-11-077-550-50
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Query Match
Best Local Similarity 42.99
Matches 12; Conservative
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LENGTH: 157
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Publication No. US20050200001

GENERAL INFORMATION:

APPLICANT: Edward Kaftan

APPLICANT: Edward Kaftan

APPLICANT: Sandy Chaplan

TITLE OF INVENTION: ASSAY SYSTEMS AND METHODS FOR DETECTING MOLECULES THAT INTERACT

TITLE OF INVENTION: MITH SK2 CHANNELS

FILLE REFERENCE: PRO142

CURRENT APPLICANT: 2004-10-28

CURRENT FILING DATE: 2004-10-28

NUMBER OF SEQ ID NOS: 11

SOOTWARE: PALENTIN VERSION 3.2
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                                                                                                                Ouery Match
37.0%; Score 60; DB 1; Length 579;
Best Local Similarity 46.1%; Pred; No. 0.27;
Matches 12; Conservative 4; Mismatches 10; Indels
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T TYBE: PRT
; ORGANISM: Rattus norvegicus
US-11-004-057-21
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; ORGANISM: Homo sapiens
US-10-975-798-4
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TYPE: PRT
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US-10-975-798-3
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18-10-97-59-64

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18-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-97-10-
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RESULT 10
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT FILING DATE: 2002-04-24
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OTHER INFORMATION: Gly residues from position 6 to 200 may be present
OTHER INFORMATION: or absent
US-11-060-659-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:synthetic poly OTHER INFORMATION: Gly flexible linker
                                                                                  APPLICANT: Lorens, James
APPLICANT: Lorens, James
APPLICANT: Holland, Sacha J.
APPLICANT: Holland, Sacha J.
APPLICANT: Au, Weiduan
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: Modulators of Angiogenesis and Tumorigenesis
FILE REFERENCE: 021044-008310US
CURRENT APPLICATION NUMBER: US/11/660,659
FRIOR APPLICATION NUMBER: US 60/545,981
PRIOR FILING DATE: 2004-02-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PARCHELIN Ver. 2.1
TITLE OF INVENTION: (KIAA0660) cDNA
SEQ ID NO 32
LENGTH: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 532, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
                    Sequence 32, Application US/11060659
Publication No. US20050250163A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desnoyers, Luc
Filvacoff, Ellen
Gao, Wei-Diang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe, Colin K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.3
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumas, Daniel
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US-11-060-659-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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Sequence 20, Application US/11065943

Sequence 20, Application US/11065943

Publication No. US20050250131A1

REMEMAL INFORMATION:

APPLICANT: VICHIER-CUERRE, SOPHIE

APPLICANT: VICHIER-CUERRE, SOPHIE

TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

TITLE OF INVENTION: WARLANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

FILE REFERENCE: 266426USOKOLP

CURRENT APPLICATION NUMBER: 205-02-5

PRIOR FILING DATE: 2004-02-27

WUMBER OF SEQ ID NOS: 106

SEC ID NOS: 106

SER ID NO 20

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PRIOR FLILNG JATES: ASS.

PRIOR APPLICATION NUMBER: 60/059113

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-09-17

PRIOR FLILING DATE: 1997-09-17

PRIOR FLILING DATE: 1997-09-17

PRIOR FLILING DATE: 1997-09-17

PRIOR FLILNG DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-17

PRIOR PLING DATE: 1997-09-18

PRIOR PLING DATE: 1997-09-18

PRIOR PLING DATE: 1997-09-19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 269;
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; Sequence 22, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
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50.0%;
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; ORGANISM: Thermus aquaticus
US-11-065-943-20
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Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 33.3
Best Local Similarity 100:
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 GGGGGGGG 257
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ORGANISM: Homo Sapien
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RESULT 14

US-11-065-943-30

US-11-065-943-30

Sequence 30, Application US/11065943

Publication No US20050250131A1

GENERAL INFORMATION:
APPLICANT: USCITAL SOPHIE

APPLICANT: VICHIER-GUEERE, SOPHIE

APPLICANT: PERRIS, STEPHANE

TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

FILE REPERENCE: 564546020CIP

TITLE OF INVENTION: UNGHER: US/11/065,943

CURRENT FILING DATE: 2005-02-25

FROM FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SEQ ID NO 30

SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/11065943

Sequence 28, Application US/11065943

Sequence 28, Application US/0050250131A1

GENERAL INFORMATION:
APPLICANT: JESTIN, JEAN-LUC

APPLICANT: JUCHIER-GUERRE, SOPHIE

APPLICANT: VICHIER-GUERRE, SOPHIE

APPLICANT: PERMS, SIEPHANE

TITLE OF INVENTION: WARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
TITLE OF INVENTION: WETHOODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

TITLE OF INVENTION: WHERE US/11/065,943

CURRENT APPLICATION NUMBER: US/11/065,943

CURRENT FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SOFTWARE: PARCHEL OF SEQ ID NOS: 106

SOFTWARE: PARCHEL OF SEQ ID NOS: 106

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Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.3%; Score 54; DB 7; Length 562; Best Local Similarity 50.0%; Pred. No. 1.4; Matches 9; Conservative 2; Mismatches 7; Indels
    CURRENT APPLICATION NUMBER: US/11/065,943
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 10/787,219
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin version 3.3
SEQ ID NO 26
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; ORGANISM: Thermus aquaticus
US-11-065-943-28
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Thermus aquaticus
US-11-065-943-26
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US-11-065-943-28
                                                                                                                                                                                                                                                                                                            LENGTH:
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US-11-065-943-24

US-11-065-943-24

SEQUENCE 24, Application US/11065943

Publication No. US20050250131A1

SERRATE USCHULE US20050250131A1

APPLICANT: USETIN, JEAN-LUC

APPLICANT: USETIN, JEAN-LUC

TITLE OF INVENTION: WATHOUS FOR OBTAINING THERMOSTABLE BNZYMES, DNA POLYMERASE I

TITLE OF INVENTION: WARLANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

TITLE OF INVENTION: WARLANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

TITLE OF SERENCE: 2664-2610SACIP

CURRENT APPLICATION NUMBER: US/11/065,943

CURRENT APPLICATION NUMBER: US/11/065,943

PRIOR PELLING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 106

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NOS: 106

SOFTWARE: PATENTIN VERSION 3.3
APPLICANT: JESTIN, JEAN-LUC
APPLICANT: VICHIERE-GUERERE, SOPHIE
APPLICANT: FERRIS, STEPHANE
TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
TITLE OF INVENTION: VARANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIES,
TITLE OF INVENTION: VARANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIES,
TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
FILE REFERENCE: 266426USOXCIP
CURRENT APPLICATION NUMBER: US, 11/065, 943
FRIOR PAPPLICATION NUMBER: US, 10/787, 219
RRIOR APPLICATION NUMBER: US, 10/787, 219
NUMBER OF SEQ. ID NOS: 106
SOFTWARE: PALENTING DATE: 2004-02-7
NUMBER OF SEQ. ID NOS: 106
SOFTWARE: PALENTING DATE: 2010 NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/11065943
| Publication Wo. US20050250131A1
| GENERAL INFORMATION:
| APPLICANT: JESTIN, JEAN-LUC
| APPLICANT: DESTIN, JEPHANE
| APPLICANT: FERRIS, SCPHIE
| APPLICANT: FERRIS, STEPHANE
| TITLE OF INVENTION: WETHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
| TITLE OF INVENTION: WARDAYS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
| TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
| FILE REPERENCE: 266426USOXCIP
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33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels
Matches 9; Conservative 2; Mismatches 7; Indels
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; ORGANISM: Thermus aquaticus
US-11-065-943-22
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ORGANISM: Thermus aquatious
US-11-065-943-24
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Sequence 32, Application US/11065943
; Sequence 32, Application US20050250131A1
; Publication No. US20050250131A1
; Publication No. USZU050250131A1
; GENERAL INFORMATION:
APPLICANT: JESTIN. JEAN-LUC
APPLICANT: JESTIN. JEAN-LUC
TITLE OF INVENTION: WAITHORS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
TITLE OF INVENTION: WAITHORS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
TITLE OF INVENTION: WHORER: US/11/065,943
CURRENT APPLICATION NUMBER: US/11/065,943
CURRENT PILING DATE: 2005-02-25
PRIOR FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PALENTIN VETSION 3:3
SEQ ID NO 32
LENGTH: 562
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33.3%; Score 54; DB 7; Length 562;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 7; Indels
                                                                                                                Query Match 33.3%; Score 54; DB 7; Length 562; Best Local Similarity 50.0%; Pred. No. 1.4; Matches 9; Conservative 2; Mismatches 7; Indels
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; ORGANISM: Thermus aquaticus
US-11-065-943-32
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-30
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November 23, 2005, 22:00:32 ; Search time 242.667 Seconds (without alignments) 2554.189 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum DB seq length: 200000000
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93
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	PTH		Aaa51731 PTH funct	Aat73910 Synthetic					Adj65858 PTH pepti	Adw14375 Human par	Adg93260 Novel exp	Aat34865 Plasmid p	Adg93181 Novel exp	Adj65859 PTH prote	Adj65913 Tandem po	Adf90345 Chimeric		Adj87051 Nucleotid	Adg93252 Novel exp
SUMMARIES	ΩI	AAA51729	AAA51730	AAA51731	AAT73910	ADG93179	ADJ65857	ADW14377	ADG93180	ADJ65858	ADW14375	ADG93260	AAT34865	ADG93181	ADJ65859	ADJ65913	ADF90345	ADJ65899	ADJ87051	ADG93252
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	Score	93	83.4	73.8	71.2	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	69.6	69.6	69.6	69.6	69.6	9.69
	Result No.		7	٣	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.

PTH	Adj65900 PTH DNA 8			Adj65917 Tandem po	Adf90347 Chimeric	DNA end	Adv69494 Human par		Adg48030 Human PTH	Adg48059 Human PTH	Adg68786 Human mut	Aaq89920 Recombina	Aat80383 rPTH codi	Aaq89923 Expressio	Adw80822 DNA encod	PCpB-		-	Aaa51453 PCpB-ALY-	AaaS1459 PCpB-APR-		AaaS14S7 PCpB-DQVD	Aaa51458 PCpB-DFIA	Aaq55301 Truncated	Aaq55302 gp55-Asn-	
12 ADJ65901	12 ADJ65900	2 AAT34866	12 ADJ65915	12 ADJ65917	~	6 AAS19702	13 ADV69494	13 ADV69502	12 ADG48030	12 ADG48059	12 ADG68786	2 AAQ89920		2 AAQ89923	13 ADW80822			3 AAA51454	3 AAA51453	3 AAA51459	3 AAA51456	3 AAA51457		2 AAQ55301		
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74.8	74.8	74.8	74.8		74.8	74.8	73.1	73.1	73.1	73.1	73.1	68.6	68.6	68.6	6.99	64.5	64.5	64.5	64.5		64.5	•				
9.69		σ		σ	6	9.69		69	68	68	68	n	m	63.8	N	9	09	9	9	09	9	9	9	2	57.4	
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44		

## ALIGNMENTS

PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis; ss. PTH functional domain conjugate peptide PG5 coding sequence. Gardella TJ, Kronenberg HM, Potts JT, Jueppner H; Location/Qualifiers
1. .93
/\*tag= a
/product= "PG5" AAA51729 standard; RNA; 93 BP. 99WO-US031108. 98US-0114577P. 31-OCT-2000 (first entry) (GARD/) GARDELLA T J. (KRON/) KRONENBERG H M. (POTT/) POTTS J T. (JUEP/) JUEPPNER H. WPI; 2000-452384/39. P-PSDB; AAY96973. WO200039278-A2 30-DEC-1999; 31-DEC-1998; Homo sapiens. Synthetic. 06-JUL-2000. AAA51729; RESULT 1 AAA51729 Key 

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RESULT 3
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                                                  Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (FFH), L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHPP which avoids the need for regular injections to treat osteoporosis
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Pred. No. 10
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1. .93
                   Claim 14; Fig 1; 119pp; English
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/product= "PG7"
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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P-PSDB; AAY96975.
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JUEPPNER H.
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Synthetic.
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(POTT/) E
(JUEP/)
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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHPP which avoids the need for regular injections to treat osteoporosis
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linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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Pred. No. 2.5e-19;
0; Mismatches 6; Indels
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                                                                                    Claim 14; Fig 1; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.5;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-452384/39.
P-PSDB; AAY96974.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200039278-A2
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Compounds of the structure or formula S-(1), n-B, R 1-S-(1), n-R or S-(1), n-R or S-(1), are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH): 1 is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-receptor signal sequence; and R is (a portion of) PTH-1 receptor capal sequence; and R is (a portion of) PTH-1 receptor capal sequence; and sed for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone canodramation, bone reacorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein; recombinant production; endoproteinase LysC; ds.
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/note= "5' end of complementary strand overhangs 3' end
of present strand by sequence 5'-TCGA-3'"
6. .152
          New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic oligonucleotide encoding linker and PTH 1-37.
                                                                                                                                                                                                                                                                                                                                                                                Sequence 93 BP; 18 A; 14 C; 35 G; 0 T; 26 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GUUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                   Claim 14; Fig 1; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT73910 standard; DNA; 152 BP
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nes 81; Conservative
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30-JAN-1998
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                                                                                                                                                                             The present sequence, which encodes a linker and the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII fragment of pSAM-CORE, which contains the Met (13-139) streptavidin (SA) sequence, to give pSA-EK-PTH. pSA-EK-PTH and the LacIg repressor plasmid pUBS500 were used to transform E. coli K12 RM82. The transformants were grown, with IPTG induction, in medium containing knamycin and amplicilin. Cells were harvested, lysed and isolated inclusion bodies solubilised in guanidine hydrochloride, and renatured by dilution in pH 7 phosphate buffer. The solution was clarified and the supernatant concentrated and purified on a column of immobilised iminobiotin. The purified material was incubated with endoproteinase LysC and the PTH 1-37 fragment released, recovered by SA fragment removal on an iminobiotin column followed by chromatography on a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fractogel and reverse phase HPLC. The composition of the Lyg cleaves the fusion protein rapidly and completely, exclusively at the Lyg residue in the linker, i.e. not at Lyg residues in SA. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
                                                                           Recombinant production of peptide(s) as fusions with streptavidin attached via cleavable linker - especially for urotropin and parathyroid hormone production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel expression cassette-related polypeptide-encoding DNA SeqID60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 71.2; DB 2; Length 152; Pred. No. 5.7e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression cassette, high yield polypeptide production;
tandem polypeptide; inclusion body; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::|||:|||:|||:|||:|||||||::
TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luan P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                     Example 2; Fig 2; 37pp; German.
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Best Local Similarity 65.2%;
Matches 60; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG93179 standard; DNA; 102
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HARLEY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-035128/03
                                WPI; 1997-289290/26.
P-PSDB; AAW21946.
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Kopetzki E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG93179;
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The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PrH 1-34 peptide (ADWH4376) severing by Pro endopeptidase to form PTH 1-34 peptide (ADWH4378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the PTH 1-34 peptide.
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                                                                                                                                                                                                                                                                   2 cuguuccgaaauccagcugaugcacgguggugguggugguggugguggaacuccauggaacgug
                                                                                                                                                                                                                                                                                                 2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
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                                                                                                                                                        Query Match
Best Local Similarity 63.0%; Pred. No. 1.9e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human parathyroxin PTH 1-34 peptide encoding DNA SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; parathyroxin; recombinant protein; protein engineering.
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                                                                                                           Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;
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TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
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es 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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ADW14377
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                                                                                                                                                                                                             This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide with may be produced using the expression cassette of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                        New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ery Match 74.8%; Score 69.6; DB 12; Length 102; st Local Similarity 63.0%; Pred. No. 1.9e-14; tches 58; Conservative 20; Mismatches 14; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 102 BP; 30 A; 24 C; 22 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGAATGGCTGCGTAAAAACTGCAGGACGTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 33; 132pp; English.
                                                                                                                                                              Disclosure, SEQ ID NO 60; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTH peptide coding sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ65857 standard; DNA; 102 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2002; 2002US-0383212P.
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P-PSDB; ADJ65837.
           P-PSDB; ADG93159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
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ADG93180 RESULT

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The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a peptide which may be used in the construction of a tandem polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CUGUIUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
                                                                                                                                                                                                                                                                                                                                                                                         New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human parathyroxin Gly-Ser-Pro-PTH 1-34 peptide DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; parathyroxin; recombinant protein; protein engineering
expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.8%; Score 69.6; DB 12; 63.0%; Pred. No. 1.9e-14; ive 20; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGAATGGCTGCGTAAAAACTGCAGGACGTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 34; 132pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-2001; 2001CN-00142627.
                                                                                                                                                                                                                      24-MAY-2002; 2002US-0383212P.
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                                                                                                                                                                               23-MAY-2003; 2003WO-US016645.
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nes 58; Conservative
                                                                                                                                                                                                                                                        (REST-) RESTORAGEN INC
                                                                                                                                                                                                                                                                                                                                    WPI; 2004-035129/03.
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                                                                                                   WO2003100022-A2
                                                                                                                                                                                                                                                                                                   Peng L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                             Xia Y,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                   Novel expression cassette-related polypeptide-encoding DNA SeqID61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
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74.8%; Score 69.6; DB 12; Length 111;
Best Local Similarity 63.0%; Pred. No. 1.9e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0.
                                                                                                                                                                                                                    expression cassette; high yield polypeptide production;
tandem polypeptide; inclusion body; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xia Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luan P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTH peptide coding sequence #2.
                                                                 ADG93180 standard; DNA; 111 BP.
                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2003; 2003WO-US016643.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harley S, Williams JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REST-) RESTORAGEN INC. (HARL/) HARLEY S.
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P-PSDB; ADG93160.
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                                                                                                                                                                                    The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-TPH 1-34 peptide (ADWH4376) sevaring by Pro endopeptidase to form PTH 1-34 peptide (ADWH4378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the Gly-Ser-Pro-PTH 1-34 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 cugurucceaaauccagcugaugcacguggugguggugguggucugaacuccauggaacgug 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 70
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                      Production of reorganized human parathyroid hormone 1-34 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression cassette; high yield polypeptide production; tandem polypeptide; inclusion body; gene; ds; PTH.
                                                                                                                                                                                                                                                                                                                                        Sequence 111 BP; 31 A; 28 C; 25 G; 27 T; 0 U; 0 Other;
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TTGAATGGCTGCGTAAAAACTGCAGGACGTT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 141; 157pp; English.
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                                                                                                                                               Claim 3; SEQ ID NO 1; 25pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2003; 2003WO-US016643.
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                                         WPI; 2004-099606/11.
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                                                               P-PSDB; ADW14376
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  Xiu C,
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Best Local S
  Chen C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  61
in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a PTH peptide which was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A portion (AAT34865) of plasmid pBN1:PTH(1-34)C-1c comprises DNA coding for a fusion protein (AAR87867) composed of the C-terminal end of human carbonic anhydrase II joined by an intraconnecting peptide (including a thrombin cleavage site) to amino acids 1-34 of PTH (AAR98966), followed by a Cys residue and C-terminal sequence. The complete construct can be expressed in B. coli transformants. The intraconnecting peptide and C-terminal Cys residue enable the recombinant protein construct to be selectively reacted to produce C-terminal carboxamidated PTH(1-34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of C-terminal alpha-carboxamidated peptide(8) - by cleavage and transpeptidation of recombinant multicopy peptide(8) or fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 cugurucceaaauccagcugaugcacggugguggugguggucugaacuccauggaacgug
                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                              Query Match 74.8%; Score 69.6; DB 12; Length 117; Best Local Similarity 63.0%; Pred. No. 1.9e-14; Matches 58; Conservative 20; Mismatches 14; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "hCA-linker-PTH(1-34)Cys fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pBN1:PTH(1-34)C-1c portion encoding PTH(1-34)Cys.
                                                                                                                                                                                                                 Sequence 117 BP; 35 A; 27 C; 25 G; 30 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 168 BP; 41 A; 44 C; 42 G; 41 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heriksen DB, Holmquist B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::|||:|||:|||:|||:|||||:|||||::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT34865 standard; cDNA; 168 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US015799
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/product= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BION-) BIONEBRASKA INC.
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P-PSDB; AAR98967.
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The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a protein which may be used in the construction of a tandem polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUGUTUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression cassette; tandem polypeptide; inclusion body;
                                                                                                                                                                                                                                               expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tandem polypeptide-encoding expression cassette #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.8%; Score 69.6; DB 12; 63.0%; Pred. No. 2.4e-14; ive 20; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGAATGGCTGCGTAAAAACTGCAGGACGTT 93
62 TTGAATGGCTGCGTAAAAACTGCAGGACGTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 35; 132pp; English.
                                                                                              ВЪ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2002; 2002US-0383212P
                                                                                                                                                                                                             PTH protein coding sequence.
                                                                                              ADJ65859 standard; DNA; 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ65913 standard; DNA; 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REST-) RESTORAGEN INC.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ADJ65839
                                                                                                                                                                                                                                                                                                                                              WO2003100022-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peng L;
                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                                                       06-MAY-2004
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                                                                                                                                    ADJ65859;
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Matches
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                                                           RESULT 14
ADJ65859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CUGUIUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCGUGAACUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CIGITITICIGAAATCCAGCIGATGCACAACCTGGGTAAACACCCTGAACTCTATGGAACGTG
                                                                                                CUGULUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Novel expression cassette-related polypeptide-encoding DNA SeqID62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
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                     Length 168;
                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression cassette; high yield polypeptide production;
tandem polypeptide; inclusion body; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;
                       DB 2;
                     ; Score 69.6; DB 2;
; Pred. No. 2.1e-14;
20; Mismatches 14
                                                                                                                                                                                             ::|||:|||:|||:|||:|||||||||||::
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                                                                                                                                                                         62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 62; 157pp; English.
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                                                                                                                                                                                                                                                                                                            ADG93181 standard; DNA; 252 BP.
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                       74.8%;
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                           58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESTORAGEN INC
HARLEY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-035128/03.
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                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                     11-MAR-2004
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Harley S,

(REST-) (HARL/)

Query Match

Matches

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ADG93181;

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Matches

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Gaps

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Length 252; Indels 61

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The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence represents an expression cassette which encodes a tandem polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                            New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
74.8%; Score 69.6; DB 12; Length 264;
Best Local Similarity 63.0%; Pred. No. 2.4e-14;
Matches 58; Conservative 20; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 264 BP; 72 A; 67 C; 64 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 89; 132pp; English.
inclusion body fusion partner; gene; ds.
                                                                                                                                                                       24-MAY-2002; 2002US-0383212P.
                                                                                                                                      23-MAY-2003; 2003WO-US016645.
                                                                                                                                                                                                         (REST-) RESTORAGEN INC.
                                                                                                                                                                                                                                                                            WPI; 2004-035129/03.
P-PSDB; ADJ65912.
                                                                   WO2003100022-A2.
                                                                                                                                                                                                                                         Xia Y, Peng L;
                                 Unidentified
                                                                                                    04-DEC-2003
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62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93 ::|||:|||:|||:||||:||| 65 TIGAATGGCTGCGTAAAAACTGCAGGACGTT 96 ò g

Search completed: November 23, 2005, 23:00:14 Job time : 244.667 secs

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November 23, 2005, 22:35:17; Search time 1177.67 Seconds (without alignments) 4488.911 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                              11766282
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                               5883141 segs, 28421725653 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM nucleic - nucleic search, using sw model
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93
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Maximum DB seq length: 200000000
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1: 9b ba:*
2: 9b_in:*
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gb_pl: *
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description			BD266834 PTH funct	AR269042 Sequence	AR005132 Sequence	AR005133 Sequence	AR177779 Sequence	AR177780 Sequence		BD234383 Recombina	BD234385 Recombina	BD234386 Recombina	BD234384 Recombina		BD234387 Recombina	BD234388 Recombina	BD234389 Recombina	A36847 Sequence 1
SUMMARIES	{	ID	BD266832	BD266833	BD266834	AR269042	AR005132	AR005133	AR177779	AR177780	AR043797	BD234383	BD234385	BD234386	BD234384	BD234390	BD234387	BD234388	BD234389	A36847
	1	. DB	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
	:	Match Length DB	93	93	93	258	141	141	141	141	207	405	408	408	411	414	417	423	435	717
	Query	Match	100.0	89.7	79.4	71.4	68.6	9.89	9.89	68.6	9.89	64.5	64.5	64.5	64.5	64.5	64.5	64.5	64.5	61.7
	,	Score	93	83.4	73.8	66.4	63.8	63.8	63.8	63.8	63.8	9	9	9	9	9	9	9	9	57.4
	Result	No.	7	7	٣	4	ഗ	9	7	ω υ	6	10	11	12	13	14	15	16	17	18

100.0%; Score 93; DB 6; Length 93;

Query Match

ORIGIN

1. .93 /organism="synthetic construct" /mol type="genomic RNA" /db\_xrefe"taxon:32630"

source

A36849 Sequence 3 AR027046 Sequence B05575 DNA encodin AR027011 Sequence AR027044 Sequence AR030635 Sequence B05658 DNA encodin B3594 Sequence B05673 DNA encodin B3594 Sequence B05671 DNA encodin B3595 Sequence B05671 DNA encodin B3596 Sequence B05671 DNA encodin B3596 Sequence B0571 Sequence B017013 Process f BD17013 Process f BD17021  Process f	linear PAT 17-JUL-2003 , derivatives thereof and	T. and Jueppner, H.	G,JOHN T POTTS,HARALD PI 8/00,A61P5/18,A61P19/08, PC 19/00,C12N1/15,C12N1/19, PC /00,C12N5/00,A61K37/02 CC fied PTH sequence FH Key al Sequence'.
A36849 AR027046 B05655 AR027041 AR027041 AR027041 AR030635 AR168173 E05658 E05673 E05673 E05673 E05671 E05672 E017019 E017019 E017019 E017019 E017019 E017019	ALIGNMENTS ALIGNMENTS 93 bp RNA domain conjugate peptides	BD266832 BD266832.1 GI:33076600 JP 2002533115-A/1. synthetic construct synthetic construct synthetic construct other sequences; artificial sequences.  ( bases 1 to 93) Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Juepp PTH functional domain conjugate peptides, derivative novel tethered ligand-receptor molecules Patent: JP 2002533115-A 1 08-OCT-2002; THE GENERAL HOSPITAL CORP OS Artificial Sequence PN JP 2002533115-A/1	08-0CT-2002 31-DEC-1999 JP 2000591171 31-DEC-1998 US 60/114577 THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTT: THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTT: THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTT: TABLES J GARDELLA, AGIK45/00, AGIK48/00, AGIP5/18 P19/10, AGIRA3/00, CO7K14/635, CO7K14/72, CO7K19/00, C12N1/1 N1/21, C12NS/10, G01N33/15, G01N33/50, C12N15/00, C12N1/1 LOCATION/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers
56.6 56.7 56.7	tional thered	BD266832 GI:33076600 BD266832.1 GI:33076600 BD266832.1 GI:33076600 Bynthetic construct synthetic construct other sequences; artificial I (bases 1 to 93) Gardella, T.J., Kronenberg, H. FUH functional domain conjug novel tethered ligand-recept patent: JP 2002533115-A 1 08 THE GENERAL HOSPITAL CORP OS Artificial Sequence N JP 2002533115-A/1	PD 08-0CT-2002 PF 30-DEC-1998 US 60/11457 PI THOMAS J GARDELLA, HENRY M JUEPPIRR PC C12N15/09, A61K38/00, A61K45 A61P19/10, PC A51P43/00, C07K14/635, C07K1 C12N1/21, C12N1/21, Description of Artificial Seque Location/Qualifiers FT Source 1.0cation/Qualifiers 1.93 FT Location/Qualifiers
19 20 20 20 20 20 20 20 20 20 20 20 20 20	RESULT 1 BD266832 LOCUS DEFINITION PL	ACCESSION BE VERSION BE KEYWORDS JE SOURCE 87 ORGANISM 87 ORGANISM 87 TITLE PE TITLE PE TOURNAL PE COMMENT OF	PP PR PR PC PC PC PC PC PC PC PC PC PC PC PC PC

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

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RESULT 2 BD266833

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CIZNIS/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PCA61P19/10,
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                                                            syntherectic construct
other sequences, artificial sequences.

1 (bases 1 to 93)
Gardella T.J. Kronenberg, H.M., Potts, J.T. and Jueppner, H.

PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules
patent: JP 2002533115-A 3 08-0CT-2002;
THE GENERAL HOSPITAL CORP
OS Artificial Sequence
PN JP 2002533115-A)
PP 30-DEC-1909 JP 2000591171
PR 31-DEC-1909 UB 2000591171
PR 31-DEC-1909 UB
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PR 31-DEC-
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Unclassified.
1 (bases 1 to 258)
Jung, E.-K., Park, D.-H. and Chung, S.-I.
Recombinant expression vector of human parathyroid hormone
Patent: US 6500647-A 26 31-DEC-2002;
Mogam Biotechnology Research Institute, Kyonggi-Do;
KRX;
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    .93
    Organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

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/organism="unknown"
/mol_type="genomic DNA"
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PR 31-L
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Th functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules.
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PTH functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules.
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PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: modified PTH sequence FH Key
Location/Qualifiers
                                                                                                                        1 GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGU 60
                                                                                                                                                                 1 GCTGTTTCCGAAATCCAGCTGATGCACGGTGGTGGTGGTGGTCGTGAACTCCATGGAACGT 60
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/organism='Artificial Sequence'.
Location/Qualifiers
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ilarity 68.8%; Pred. No. 2.6e-17;
Conservative 23; Mismatches 6; Indels
Best Local Similarity 74.2%; Pred. No. 1.4e-20;
Matches 69; Conservative 24; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                           61 GUUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
|::|||:|||:|||:|||:||||::
61 GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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JP 2002533115-A/3.
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RESULT 3 BD266834 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

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AR005132
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KEYWORDS
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                   62
                                                                                       56;
                                                                                                                                                                        1 (bases 1 to 141)
Holladay,L.A. and Oldenburg,K.R.
Method for increasing the electrotransport
Patent: US 5747453-A 5 05-MAY-1998;
Location/Qualifiers
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Holladay,L.A. and Oldenburg,K.R.
Method for increasing the electrotransport
Patent: US 5747453-A 3 05-MAY-1998;
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| | :::||||||:||:||:|| | ||:||
CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGAATGGCTGCGTAAAAACTGCAGGATGTT
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                                                       CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                                                                          TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTTTCGGAAATCCAGCTTATGCATAACCTGGGTAAACATCTGAACTCGATGGAACGTG 61
TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26
                     UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
                                          Conservative
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                                                                                                                                          /organism="unknown"
/mol_type="unassigned
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61.5%;
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Pred. No. 1.2e-10;
B; Mismatches 17;
                                                                                     Score 63.8; DB 6;
Pred. No. 1.2e-10;
8; Mismatches 17;
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AR177779
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AR043797
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Sequence 3
AR177779
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AR177780
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                                                                                                                                                                                                                                             1 (bases 1 to 141)
Holladay,L.A. and Oldenburg,K.R.
Method for increasing the electrotransport
Patent: US 6313092-A 5 06-NOV-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 141)
Holladay, L.A. and Oldenburg, K.R.
Method for increasing the electrotransport
Patent: US 6313092-A 3 06-NOV-2001;
       AR043797
Sequence 8 from patent US
AR043797
AR043797.1 GI:5964805
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                                                                                      TIGAAIGGCIGCGTAAAAACTGCAGGACGI
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/mol_type="unassigned
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; Pred. No. 1.2e-10;
18; Mismatches 17;
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Pred. No. 1.2e-10;
8; Mismatches 17;
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Best Local Similarity
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other sequences; artificial sequences.

other sequences; artificial sequences.

RS Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

REOMBRIANT STATEMENT S
                                                                                                           293
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: |||:|||:|||:|| || || |:|||||| ||::
153 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 CCGTTTCCGAAATCCAGCTGCTGCACACCTGGGTAAACACCTGAACTCCCTCGAGCGTG
                                                                                                        2 CUGUJUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
|:|:::| ||||:|| ||:|| ||:||
93 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 352
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1 (bases 1 to 207)
Oldenburg, K.R. and Selick, H.E.
Compounds with PTH activity
Patent: US 5814603 A 8 29-SEP-1998;
                                                                                                                                                                                                                   Similarity
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synthetic construct
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BD234383.1 GI:33044153
JP 2002533072-A/4.
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Recombinant synthesis of beta-lipotropin and other peptides.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
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1. .207
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                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                   Score 60; DB 6; Le
Pred. No. 2.5e-09;
9; Mismatches 20;
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DEFINITION
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Matches 53
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synthetic construct

fish synthetic construct

other sequences; artificial sequences.

1 (Dases 1 to 408)

Relegion 15. Hershberger C.L., Larson, J.L. and Menke, M.A.

Recombinant synthesis of beta-lipotropin and other peptides

patent: JP 2002533072-A 7 08-OCT-2002;

ELI LILLY AND CO

OS Artificial Sequence

PD 08-OCT-2002

PD 08-OCT-2002

PD 15-DEC-1998 US 60/113058

PR 21-DEC-1998 US 60/113058

PR 1-DEC-1998 US 60/113058

PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,

PO C12N15/09, CO7K14/67, C07K19/00, C12N1/15, C12N1/21 PC

C12N15/10, C12N9/50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATENT: JP 2005333072-A 6 08-OCT-2002;

ELI LILLY AND CO
OS ATTIFICIAL Sequence
PN JP 2002533072-A/6

PP 15-DEC-1999 JP 2000589671

PP 21-DEC-1999 US 60/113058

PR 21-DEC-1999 US 60/113058
PR 21-DECADD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,
PI MICHAEL ANDREW MERKE
PC C12N15/09, C07K14/67, C07K19/00, C12N1/15, C12N1/19, C12N1/21 PC
C12N5/10, C12N9/50
PC C12P21/02, C12N15/00, C12N5/00
PC Description of Artificial Sequence: PCpB-IEGR-hPTH fusion FH
LOCATION (A). (396).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
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53; Conserva
                                                                                                                                                                                                                                                                                                                   BD234386.1 GI:33044156
JP 2002533072-A/7.
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1 (bases 1 to 408)

Hale, J.E., Hershberger, C.L., Larson, J.L.
Recombinant synthesis of beta-lipotropin
Patent: JP 2002533072-A 6 08-OCT-2002;
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JP 2002533072-A/6.
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/mol_type="genomic DNA"
/db_xref="taxon;32630"
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RS Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

RS Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

RECombinant synthesis of beta-lipotropin and other peptides

Reco
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359
                                                                                                               299 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG
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                                 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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other sequences; artificial sequences.
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TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT 390
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
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57.6%;
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57.6%; Pred. No. 2.5e-09;
tive 19; Mismatches 20
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1 (bases 1 to 414)

Hale, J.E., Hershberger, C.L., Larson, J.L. and Recombinant synthesis of beta-lipotropin and Patent: JP 2002533072-A 11 08-OCT-2002;

ELI LILLY AND CO
OS Artificial Sequence
PN JP 2002533072-A/11

PD 08-OCT-2002

PF 15-DEC-1999 JP 2000589671

PR 21-DEC-1998 US 60/113058

PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGI
PI MICHAEL ANDREW MENKE
PC C12N15/09, CO7K14/67, CO7K19/00, C12N1/15

PC C12N5/10, C12N15/00, C12N5/00

PC C12P21/02, C1N15/00, C12N5/00

PC C12N5/02, CN15/02, C1N5/00

PC C12N5/02, CN15/02, C1N5/02, CN15/02, CN15/02
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Recombinant synthesis of beta-lipotropin and other peptides.
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milarity 57.6%;
Conservative 19
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C12P21/02,C12N15/00,C12N5/00
Description of Artificial Sequence: PCpB-APR-hPTH fusion FH
Location/Qualifiers
CDS (4) . (402).
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21-DEC-1998 US 60/113058
JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON, MICHAEL ANDREW MENKE
C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
                                                                                                                                       15-DEC-1999 JP 2000589671
21-DEC-1998 US 60/113058
JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON, MICHAEL ANDREW MENKE
C12N15/09, C07K14/67, C07K19/00, C12N1/15, C12N1/19, C12N1/21 PC
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Pred. No. 2.5e-09;
.9; Mismatches 20;
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other peptides
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Key

Location/Qualifiers

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
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W19763
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W3966 zb34c06.r1
W3966 zb28b12.r1
W39708 zc10d12.r1
W31798 zb96d06.r1
W31998 zb96d06.r1
W31998 zb96d06.r1
W31977 zc07a12.r1
W56235 zc01e11.r1
W56235 zc01e01.r1
W56120 zc56h06.r1
W39702 zb35h03.r1
W39202 zb35h03.r1
W39202 zb35h03.r1
BG19856 RST17929
A105197 cy29c05.x
BX106232 BX106232
BX106232 BX10523
BX103059 BX103059
A3372113 EST83988 Hu
W52945 zc03h08.r1
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    AI031553 ow48c08.x
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DN348441	DN348349	DN348316	DN347653	DN348165	DN348145	DN347706	DN348206	DN348137	DN350926	DN348558	DN347146	DN347234	DN347142	DN347334	DN346863	DN347081	DN346969	DN347054	4920	DN348158	766	AA843141
LIB3578-0	LIB3578-0	LIB3578-0	LIB3578-0	LIB3578-0	LIB3578-0	LIB3578-0	LIB3578-0			LIB3578-0	T183578-0	α	Ϋ́	٠								

## ALIGNMENTS

	FEATURES source		COMMENT	TITLE	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 W19763 LOCUS DEFINITION ACCESSION
/Organishm=nomo bapiens: /mol type="manNa" /mol type="manNa" /db_xref="GDB:1249362" /db_xref="GDB:1249362" /db_xref="taxon:9606" /clone="IMAGE:305952" /tissue_type="parathyroid tumor" /dev_stage="adult" /lab_host="DH10B (ampicillin resistant)" /clone_iD="Soares_parathyroid tumor_NbHPA" /note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I;	High quality sequence stop: 222.  High quality sequence stop: 222.  Location/Qualifiers 1. 324  //coststant/locations/	rex: 314 286 1810 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. See primer: mob REGALET	Inpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	T Project	Hominidae, Homo.  Hominidae, Homo.  1 (bases 1 to 324)  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,	W19763.1 GI:1295880 EST. Homo sapiens (human) Homo sapiens (human) Homo sapiens (chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Mammaiia. Rutheria. Ruarchontrodlires: Primates; Catarrhini;	W19763  ZD39c01.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:305952 5' sīmilar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.

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Query Match
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                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1800
Email: estiwation wustl.edu
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: mob.REGA+ET
Seg primer: mob.REGA+ET
High quality sequence arco.
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120 TAGAATGGCTGCGTAAGAANCTGCAGGATGT 150
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 352)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Hillier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Tennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739062 352 bp mRNA linear EST 15-MAY-1996 zb34c06.rl Soares parathyroid tumor NbHPA Homo sagiens cDNA clone IMAGE:305482 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W39062
W39062.1 GI:1320771
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Location/Qualifiers
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mol type="mRNA"
/db_xref="GDB:1248892"
/db_xref="taxon:9606"
/clone="IMAGE:305482"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH108 (ampicillin resistant)"
/clone_lib="Soares_parathyroid tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site 1:
Site_2: Eco RI; 1st strand cDNA was primed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.0%;
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Pred. No. 2.9e-05;
5; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
COMMENT
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VERSION
KEYWORDS
SOURCE
ORGANISM
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W38966
LOCUS
DEFINITION
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AUTHORS
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RESULT 2 W39062 LOCUS DEFINITION

ACCESSION VERSION

KEYWORDS ORGANISM

밁 5 В Ş

Local

JOURNAL COMMENT

FEATURES

source

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Query Match
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Contact: Wilson RK
Washington University School of 4444 Forest Park Parkway, Box 81
Tel: 314 286 1800
Fax: 314 286 1810
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376 bp mRNA linear EST 15-MAY-1996
zb28bl2.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE:304895 5' sImilar to gb:V00597 PARATHYROID HORMONE PRECURSOR
(HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: mob.REGALET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 275
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                                  /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9506"
/db xref="taxon:9506"
/clone="IMAGE:304895"
/tissue_type="parathyroid tumor"
/tissue_type="parathyroid tumor"
/dev stage="adult"
/dev stage="adult"
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/clone_lib="Soares_parathyroid gland; Vector: pT7T3D
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site 1: Not
Site_2: ECORI; 1st strand cDNA was primed with a N
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x 8501, St. Louis,
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a Not I -
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 cugurucceaaauccaecueauccacegueguegueguegucueaacuccauegaacgue 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1995)
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Mammalia; Eutheria;
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TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 262
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                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/db xref="GDB:1259569"
/db xref="taxon:9606"
/clone="IMAGE:321911"
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/clone_lib="Soares_parathyroid_tumor_NbHPA"
/clone_lib="Soares_parathyroid_gland; Vector: pT7T3D
/pharmacia) with a modified_polylinker; Site_1: Not_I;
Site_2: Eco_RI; 1st_strand_cDNA_was_primed_with a Not_Site_2: Eco_RI; 1st_strand_cDNA_was_primed_with a Not_Site_2: Eco_RI; 1st_strand_cDNA_was_primed_with_a Not_Site_2: Eco_RI; 
tissue_type="parathyroid tumor"/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Hultman, M., Kucaba, T., Lacy, M., Le, M., Che, N., Mardis, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
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Contact: Wilson RK
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1 (bases 1 to 416)
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zb96d06.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone
IMAGE:320651 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 771 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W31998
                                                                                                                                                                                                                                                                                                                                                                      Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                              quality sequence
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/tissue_type="parathyroid tumor"
/dev stage="adoilt"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid_gland; Vector: pT7T3D
(pharmacia) with a modified_polylinker; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                   mol_type="mRNA"
                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                              clone="IMAGE:320651"
                                                                                                                                                                                                             db_xref="GDB:1258309"
                                                                                                                                                                                                                                                                                               .416
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53.8%;
                                                                                                                                                                                  xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                              stop: 386.
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                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
Info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.

1 (bases 1 to 434)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Alfkin,L., Rohlfing,T., Soarses,M., Tan,F.,
Parsons,J., Alfkin,L., Rohlfing,T., Soarses,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W38764 434 bp mRNA linear EST 15-MAY-1996 zb27a07.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:304788 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W38764
W38764.1 GI:1320471
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                                                                                                                                                                                                                                                                                 primer: mob.REGA+ET
n quality sequence stop: 253
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="parathyroid tumor"
/dev stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/clone_lib="Soares_parathyroid_gland; Vector: pT7T3D
/note="Organ: parathyroid_gland; Vector: pT7T3D
/pharmacia) with a modified polylinker; Site 1: Not I;
/Site_2: Eco RI; 1st strand cDNA was primed with a Not :
                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:304788"
                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="GDB:1248198"
                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.4%;
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Pred. No. 4.8e-05;
.5; Mismatches 27;
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REFERENCE AUTHORS

COMMENT

FEATURES

/tissue\_type="parathyroid tumor"
/dev stage="adult"
/lab host="PHIOB (ampicillin resistant)"
/clone\_lib="Soares\_parathyroid\_tumor\_NbHPA"
/clone\_lib="Soares\_parathyroid\_tumor\_NbHPA"
/note="Organ: parathyroid\_gland; VecTor: pT7T3D
/pharmacia) with a modified\_polylinker; Site 1:
Site\_2: "ECO\_RI; lst strand\_cDNA\_was primed\_with

a Not Not I /db\_xref="taxon:9606" /clone="IMAGE:321068"

oligo(dT) primer

ACCESSION VERSION KEYWORDS

ORGANISM

RESULT W38764

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DEFINITION

멍 Ş B ş ORIGIN

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM TITLE JOURNAL COMMENT REFERENCE AUTHORS RESULT W56235 DEFINITION FEATURES Query Match Best Local Matches source 174 49; The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Tel: 314 286 1800
Email: est@wateon.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (Info@image.llnl.gov) for further information.
Insert Length: 865 Scd Error: 0.00
Seq primer: mob.REGA+ET. 1 (bases 1 to 450)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Clark,N., Sucaba,T., Le,M., Lennon,G., Marra,M
Holman,M., Hultman,M., Kucaba,T., Soares,M., Tan,F.,
Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and W56235 mRNA linear EST 10-OCT-1996 zc01e11.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone INACE:321068 5 similar to gb:V00597 PARATHYROID HORMONE PRECURSOR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. Homo sapiens (human) (HUMAN);, mRNA sequence. Similarity : |||:|||:|| || |:||||| |: TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 264 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG cugurucceananceaeceaecus au construction de la const Conservative /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="GDB:1258726" Location/Qualifiers 51.4%; 15; Score 47.8; DB 8; Pred. No. 4.8e-05; 5; Mismatches 27; Length 434; Marra, M., 0 233 61 0

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ACCESSION
VERSION
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W33077
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W33077

453 bp mRNA linear EST 10-OCT-1990 zc07a12.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone mage: 321598 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 871 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-Merck EST Project Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 453)
                                                                                                                                                                                                                                                                                                                                                                                               primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 367.
Location/Qualifiers
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                                                                                                                                                                                         /organism="Homo sapiens"
/mol type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:321598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
oligo(dT) primer
                    /clone lib="Soares parathyroid tumor_NbHPA"
/note="Organ: parathyroid gland; VecCor: pT7T3D
/note="Organ: parathyroid gland; VecCor: pT7T3D
/Pharmacia) with a modified polylinker; Site 1: Not 1;
Site 2: Bco RI; 1st strand cDNA was primed with a Not
                                                                                                                     /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
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Pred. No. 4.9e-05;
L5; Mismatches 27;
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FEATURES

COMMENT

JOURNAL

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DEFINITION Query Match ORGANISM Local Similarity 201 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 49; 496 bp mRNA linear EST 10-OCT zc01a03.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA cl. IMAGE:321004 5' sīmilar to gb. V00597 PARATHYROID HORMONE PRECU (HUMAN); mRNA sequence. Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 858 Std Error: 0.00 Contact: Wilson RK Washington University School of Medicine The WashU-Merck EST Project Unpublished (1995) 1 (bases 1 to 496)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Homo sapiens 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Hominidae; Homo. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens (human) W56820.1 GI:1358743 Seq primer: mob.REGA+ET Wilson, R TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 291 quality sequence stop: 424. Conservative TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH." /clone lib="Soares parathyroid tumor NbHPA" /note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Site 2: Eco RI; 1st strand cDNA was primed with /tissue type="parathyroid tumor"
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ACCESSION VERSION

KEYWORDS

REFERENCE

AUTHORS

W56820 LOCUS

RESULT

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Matches

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W19765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq_primer: mob.REGA+ET
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1 (bases 1 to 536)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rohlfing,T., Roh
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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W19765.1 GI:1295882
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Location/Qualifiers
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314 286 1810
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/dev stage="adult"
/lab host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/clone_"Organ: parathyroid_gland; Vector: pT7T3D
/pharmacia) with a modified polylinker; Site 1:
Site_2:_ECO_RI; 1st strand_cDNA_was_primed_with
                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249366"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:305956"
51.4%;
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                               51.4%;
Score 47.8; DB 8;
Pred. No. 5e-05;
Prediction 27;
                                                                  Length 536;
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ORIGIN

TITLE JOURNAL COMMENT REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT W56120 LOCUS 밁 Ş 밁 Ś FEATURES DEFINITION Matches source 249 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 189 62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92 N Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 904 Std Error: 0.00
Seq primer: mob.REGA+ET Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson. Unpublished (1995) Contact: Wilson RK Washington University School c 4444 Forest Park Parkway, Box Homo sapiens W56120.1 GI:1358009 EST. w56120 576 bp mRNA linear EST 11-OCT-1990 zc56h06.rl Soares\_parathyroid\_tumor\_NbHPA Homo sapiens cDNA clone IMAGE:326363 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR 1 (bases 1 to 576)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; The WashU-Merck EST Project W56120 Wilson, R. fominidae; Homo sapiens (human) (HUMAN);, mRNA sequence. CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG cugurucceaaanccaecueauecacecueguegueguegueguegaacuccauegaaceue quality sequence stop: 433. Location/Qualifiers Conservative /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="GDB:1260565" /db\_xref="taxon:9606" clone="IMAGE: 326363" Homo 15; of Medicine x 8501, St. Louis, 279 Indels ð 63108 Marra, M., EST 11-OCT-1996 **0** 61

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                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET
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Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 400
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/tissue_type="parathyroid tumor"
/dev_stage="adult"
/dev_stage="adult"
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/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1: Not_I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249031"
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'clone="IMAGE:305621"
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Matches

49;

Conservative

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Gaps

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SOURCE
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Best Local
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113 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU
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BG198564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.

1 (Dases 1 to 721)

1 (Dases 1 to 721)

1 (Dases 1 to 721)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,

Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,

Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,

Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,

Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,

Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG198564.1 GI:13720251
                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11329013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3201 Carnegie Ave, Cleveland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Athersys, Inc.
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Athersys RAGE Library Homo
                                                                                                         /clone_lib="Athereys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
/nibraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                              'organism≃"Homo sapiens'
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                     51.4%;
                                                                                                                                                                                                                                                                           line="HT1080"
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Pred. No. 5.1e-05;
5; Mismatches 27;
Score 47.8; DB 2;
Pred. No. 5.3e-05;
5; Mismatches 27;
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sapiens cDNA, mRNA sequence.
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                                        Length 721;
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                                                                                               618 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 559
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62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92 : ||||:|||:|||:|| || |:|||||:||:||
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                                                                                                                                                    2 cueuuucceaaauccaecueauecacegueguegueguegucgaacuccauegaacegue 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/lmage.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 444.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIO51997 THE EST 10-JUL-1998 OY2905.X1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone (MAGE:1667240 3' Similar to g5:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMAN);, mRNA sequence.
AI051997
AI051997.1 GI:3307988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 741)
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                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                 Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1667240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                            51.4%;
53.8%;
                                                                                                                                                                                                                   Score 47.8; DB 1;
Pred. No. 5.3e-05;
5; Mismatches 27;
                                                                                                                                                                                                                                                                        Length 741;
                                                                                                                                                                                                                   Indels
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BX106232
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L Unpublished (2003)

L Contact: Ina Rolis

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; INAG9998U24728.

RZPDLIB; I.M.A.G.E. CDNA Clone Collection;

Human UnigeneSet - RZPDIB No.972)

http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response7ibNo-972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

Fax: +49 30 32639 111

Fax: +49 30 32639 111
                                                                                               210 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT
62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92 : |||:|||:|||:|| || |:|||||:||
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1 (bases 1 to 757)

Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.

Human UnigeneSet - RZPD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX106232 Fixed parathyroid tumor NbHPA Homo sapiens IMAGE998UZ4728; IMAGE:321911, mRNA sequence.

BX106232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: contact RZPD reference: TTCACACAGGAAACAGCTATGAC.

Ml3r, Primer sequence: TTCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/db xref="taxon:9606"
/dev stage="adult"
/lab host="Hol8 (ampicillin resistant)"
/lab host="Hol8 (ampicillin resistant)"
/clone lib="Soares parathyroid tumor_NbHPA"
/clone lib="Soares parathyroid tumor_NbHPA"
/clone lib="Soares parathyroid gland; VecTor: pT7T3D
/note="Togan: parathyroid tumor_NbHPA"
/note=
                                                                                                                                                                                                                                                                                                                                                                 TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sitee of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
                                                                                                                                                                                                                                                51.4%;
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                                                                                                                                                                                                                   Score 47.8; DB 5;
Pred. No. 5.3e-05;
5; Mismatches 27;
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s cDNA clone
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Search completed: November 24, 2005, 01:30:28 Job time : 1825 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1: /cgn2_6/ptcodata/l/ina/5_COMB.seq:*

2: /cgn2_6/ptcodata/l/ina/5_COMB.seq:*

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5: /cgn2_6/ptcodata/l/ina/H_COMB.seq:*

6: /cgn2_6/ptcodata/l/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptcodata/l/ina/PCOMB.seq:*

8: /cgn2_6/ptcodata/l/ina/RE_COMB.seq:*

9: /cgn2_6/ptcodata/l/ina/RE_COMB.seq:*
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Match
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GenCore version (c) 1993 - 2005
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                 3 US-09-463-282D-26

2 US-08-468-275-3

2 US-08-468-275-5

3 US-09-007-466-5

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3 US-09-952-980B-5

2 US-08-142-551B-8

2 US-08-133-446-58

2 US-08-133-446-23

2 US-08-133-446-23

2 US-08-133-446-32

2 US-08-689-190-3

2 US-08-689-190-3

2 US-08-689-190-3

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Query Best Matcl Qy Db Db	RESULT 1 US-09-463- Sequence Patent N GENERAL APPLICA APPLICA APPLICA APPLICA APPLICA CURRENT CURRENT CURRENT FRIOR A PRIOR A PRIOR A PRIOR A PRIOR A PRIOR B COTTUBE CURRENT	00 0 00 20202 20203 2020
/ Match Local S nes 55 2 2 62	SULT 1  Sequence 26, Application US Sequence 26, Application US Patent No. 6500647  GENERAL INFORMATION: APPLICANT: Jung, Eun-Kyung APPLICANT: Park, Doo-Hong APPLICANT: Chung, Soo IIITLE OF INVENTION: RECOMBILE REFERENCE: 0136/06626 CURRENT APPLICATION NUMBER: 2000 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-07 NUMBER OF SEQ ID NOS: 26 SOPTWARE: PATENTIN VERSION SEQ ID NO 26 LENGTH: 258 TYPE: DNA ORGANISM: Homo sapiens -09-463-282D-26	\$4\$4\$4\$4\$656577888888882222888888222
Similarity 59. Similarity 59. Si, Conservative Cuguuuccgaaaucc    :         Cuguuuccgaaaucc    :          Cugaauggcugcgua                Tigaargcugcugcgua	-282D-26 -282D-26 -26, Application US/09463282D No. 6500647 , INFORMATION: ANNT: Unng, Eun-Kyung ANT: Park, Doo-Hong ANT: Chung, Soo I CF INVENTION: RECOMBINANT EXPR EFERENCE: 0136/06626 FITAPPLICATION NUMBER: US/09/46 APPLICATION NUMBER: PCT/KR98/0 FILING DATE: 1998-06-05 FILING DATE: 1997-07-27 APPLICATION NUMBER: KR 1997-35 FILING DATE: 1997-07-27 APPLICATION SEQ ID NOS: 26 APPLICATION SEQ ID NOS: 26 APPLICATION SEQ ID NOS: 26 BRE: PatentIn version 3.1 NO 26 H: 258 DNA	51 51 51 51 51 51 51 51 51 51 51 51 51 5
71.4% 59.8% ative ahrccag   :    AARCCAG   :    GCGUAAAJ   :      :	Sation US/0946: N: Sun-Kyung Doo-Hong As of 1 N: RECOMBINANT NUMBER: US/ NUMBER: PCT/N NUMBER: RR 19: 1998-06-05 NUMBER: RR 19: 1997-07-27 NOS: 26 N version 3.1	537 537 5337 77 77 77 77 77 77 77 77 77 77 77 77
%; Score 66.4; DB 3; L %; Pred. No. 2.5e-13; 21; Mismatches 16; 21; Mismatches 16; 3CTTATGCATAACCTGGGTAAACAT AAAACTGCAGGATGTT 93 AAAACTGCAGGATGTT 93	09463282D  NANT EXPRESSION VECTOR OF  US/09/463,282D  01-20  CT/KR98/00146  05  R 1997-35230  27	2 US-08-835-231-5 2 US-08-835-231-6 3 US-09-108-661-5 3 US-09-108-661-6 3 US-09-949-016-6182 3 US-09-949-016-6782 3 US-09-949-016-11793 3 US-09-949-016-11793 3 US-09-949-016-13712 2 US-08-733-446-22 2 US-08-733-446-21 2 US-08-733-446-21 2 US-08-733-446-26 2 US-08-733-446-26 2 US-08-733-446-26 2 US-08-733-446-29 2 US-08-733-446-29 3 US-08-733-446-29 2 US-08-733-446-29 3 US-08-733-446-29 3 US-08-733-446-29 3 US-08-733-446-29 3 US-08-733-446-29 3 US-08-733-446-29 4 US-08-733-446-29 5 US-08-733-446-29
Length 258; Indels 0; Gaps 0; UCUGAACUCCAUGGAACGUG 61 : :   :   :    :  TCTGAACTCGATGGAACGTG 61	HUMAN PARATHYROID HORMONE	Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 18519, A Sequence 18519, A Sequence 1870, Appl Sequence 11793, A Sequence 11793, A Sequence 11793, A Sequence 22, Appl Sequence 23, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 28, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appli

RESULT 2
US-08-468-275-3
US-08-468-275-3
; Sequence 3, Application US/08468275
; Patent No. 5747453
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; TITLE OF SEQUENCES: 10

us-09-475-158a-14.rni

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RESULT 3

US-08-468-275-5/c

i Sequence 5, Application US/08468275

j Sequence 5, Application US/08468275

j Patent No. 5747453

i GENERAL INFORMATION:
    APPLICANT: HOLLADAY, LESLIE A.
    APPLICANT: OLDENBURG, KEVIN R.

ITITLE OF INVENTION: METHOD FOR INCREASING THE
    TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
    UNMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: ALZA CORPORATION

ADDRESSEE: ALZA CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 7..138
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 25
US-08-468-275-3
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REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0,360
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEPAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
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Best Local :
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MEDIUM TYPE: FLOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION NUMBER: US/08/468,275
APPLICATION NUMBER: US/08/468,275
ETLING DATE: 06-UUN-1995
CLASSIFICATION: 514
ATTORNET/AGENT INFORMATION:
NAME: MILLER, D. BYRON
RECITEMPATION: BYRON
ZIF: 94303-0802

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
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MOLECULE TYPE:
FEATURE:
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ADDRESSEE: ALZA CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 950 PAGE MILL
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94303-0802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 68.6%; Score 63.8; DB 2; 1 Similarity 61.5%; Pred. No. 1.7e-12; 56; Conservative 18; Mismatches 17;
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US-09-007-466-3
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Best Local
    141 base pairs nucleic acid
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ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEPAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
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Gaps
    0
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NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEPAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS: GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
APPLICANT: OLDENBURG, KEVIN R.
APPLICANT: OLDENBURG, KEVIN R.
APPLICANT: OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
INTERED: OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
INTERED: OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STREET: PALO ALTO
STREET: PALO ALTO
STREET: PALO ALTO CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILLING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION: ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/007,466 ch 68.6%; Score 63.8; DB 2; l Similarity 61.5%; Pred. No. 1.7e-12; 56; Conservative 18; Mismatches 17; , Application US/09007466 6313092 US 08/468,275 0360-0002; ARC-2349

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                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
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 Best Local Similarity
Matches 56; Conserv
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/007,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                MOLECULE TYPE:
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LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 950 PAGE
                                                                                                 TOPOLOGY: 111
                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94303-0802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
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7..138
68.6%; Score 63.8; DB 3; Length 141; ilarity 61.5%; Pred. No. 1.7e-12; Conservative 18; Mismatches 17; Indels
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25
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                                                                              DNA (genomic)
                                                                                                             single
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                                                                                                                          Matches
                                                                                                                                                      Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: HOLLAD
                                                                                                                                                                                                   LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,980
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CITY: PALO ALTO
CTATE: CALIFORNIA
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APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF E
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 496-8150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                       68.6%; Score 63.8; DB 3; Local Similarity 61.5%; Pred. No. 1.7e-12; les 56; Conservative 18; Mismatches 17;
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98
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                 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
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20-NOV-1997
V; FT.
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RESULT 7 US-08-952-980B-5/c ; Sequence 5, Application US/08952980B

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US-08-142-551B-8
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08142551B Patent No. 5814603 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING
TITLE OF INVENTION: ELECTROTRANSPORT FLUX
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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Best Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,980B
FILING DATE: 20-NOV-1997
CLASSIFICATION: 530
CLASSIFICATION: 530
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REGISTRATION NUMBER: 30,661
REGISTRATION NUMBER: 20,761
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 496-8150
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY:
                                                                                                                   STREET: 699 Prince Street CITY: Alexandria STATE: Virginia
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                                                                                                COUNTRY:
                                                                                                                                                                                 ADDRESSEE:
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56 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 26
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                                                                                                                                                                                 Doane, Swecker & Mathis
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US-08-733-446-58
Sequence 58, Application US/08733446
Sequence 50, Application US/08733446
Patent NO. 5856138
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS.
TITLE OF INVENTION: PRODUCTION THEREOF
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 07/965
EILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:

NAME: Swiss, Gerald F.

REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local S
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FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 07/898,219
FILING DATE: 12-JUN-1992
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NAME/KEY: misc feature
LOCATION: 1..51
OTHER INFORMATION: /note
OTHER INFORMATION: seque
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NAME/KEY:
LOCATION:
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NAME/KEY: misc feature
LOCATION: 70..174

OTHER INFORMATION: /not
OTHER INFORMATION: pept
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LOCATION: 175..207
OTHER INFORMATION: /note
OTHER INFORMATION: havii
OTHER INFORMATION: purif
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56; Conservative
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having six histamines that serves as a tag for the
purification of the protein on a nickel column."
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sequence that serves to direct the
inclusion bodies."
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peptide of interest"
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RESULT 10
US-10-340-484-14
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                            GENERAL INFORMATION:
APPLICANT: Stewart, Andrew F.
APPLICANT: Stewart, Andrew F.
TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501
CURRENT ELIUNG DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/347,215
PRIOR APPLICATION NUMBER: 60/347,215
PRIOR APPLICATION NUMBER: 60/353,296
PRIOR APPLICATION NUMBER: 60/353,296
                                                                                                                                                                                                                                   Sequence 14, Application US/10340484 Patent No. 6875739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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STREET: 130 W
CITY: Boston
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: NEUNER, George
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 252 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double
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APPLICATION NUMBER: 60/368,955
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGTGTCCGAGATTCAGCTGCTGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG
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                      2002-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.3%; Score 54.2; DB 2; Length 252; 54.9%; Pred. No. 4e-09; ative 18; Mismatches 23; Indels
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-340-484-14
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CLASSITE US/08/689,190

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 102
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/379,125
PRIOR FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 27
                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                    APPLICATION NUMBER: US/07/765,371
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D
REGISTRATION NUMBER: 30,901
                                                                                                                                   REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEPHAX: (617) 523-6440
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN TITLE OF INVENTION: PARATHYROID HORMONE NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN STREET: 130 Water Street
                                                                                                                                                                                                                                                                           FILING DATE:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSHIKA, Yuri
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other nucleic acid, synthesizing DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsunehiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.6%; Score 52.6; DB 3; 53.8%; Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                               US/08/016,171
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RESULT 12
US-08-733-446-23
US-08-733-446-23
(Sequence 23, Application US/08733446
Patent No. 5856128
Patent No. 5856128
PAPPLICANT: FUKUDA, Tsunehiko
PITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS AND TITLE OF INVENTION: PRODUCTION THEREOF
POWNES OF SEQUENCES: 62
CORRESPONDENCE ADDRESS: 62
CORRESPONDENCE ADDRESS: 62
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, NAME/KEY: MUTATION
; LOCATION: 7, 8, 9, 12, 15, 19, 21,
; IDENTIFICATION METHOD: S
US-08-689-190-1
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S6.5%; Score 52.6; DB 2;

Best Local Similarity 53.8%; Pred, No. 1.4e-08;

Matches 49; Conservative 18; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/402,970
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
                                                                                                          TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, GEOYGE W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 4202
TELECOMMUNICATION INFORMATION:
TELECOMOUS (617)523-3400
                                                                          TOPOLOGY: 13
                                                                                                                                                                                                                              TELEFAX:
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IDENTIFICATION METHOD:
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E: other nucleic
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                                                                          synthetic
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                                                                       US-08-733-446-56
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Best Local Similarity 53.8
Warches 49; Conservative
                                                                                                                                                                                                                                                                      NAME: NEINER, George W

REGISTRATION NUMBER: 26964

REFERENCE JOCKET NUMBER: 4202

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)523-3400

TELEPAX: (617)523-6440

TELEXX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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Query Match
56.6%; Score 52.6; DB 2; Length 252;
Best Local Similarity 53.8%; Pred. No. 1.4e-08;
Matches 49; Conservative 18; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: FUKUDA
                                                                                                                                                                                                  LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYDE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-OCT-1996
FILING DATE: 18-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                         NAME/KEY:
LOCATION:
NAME/KEY:
LOCATION:
                                                                                      NAME/KEY: mutation LOCATION: 103...105 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: DAVID G
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
: |||:|||:|||:|| || :||| :|| || :||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5, Application US/08733446
5856138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 Water Street
                                                                                                                                                                CDS
                                                                                                                                                 1..252
                                                                                                                                                                                                    other nucleic acid, synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), Tsunehiko

HUMAN PARATHYROID HORMONE MUTEINS AND

HERODUCTION THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.6%; Score 52.6; DB 2; 53.8%; Pred. No. 1.4e-08; tive 18; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/402,970
                                                                                                                                                                                                                                                                                                                                                                                                             42025
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RESULT 14
US-08-835-231-34
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                                                  ; NAME/KEY:
; LOCATION:
US-08-835-231-34
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Patent No. 5
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 4161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/835,23
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
                                                                                                                                                                                                                                                                                                TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KURIYAMA, Masato
APPLICANT: KOYAMA, No. 5861284uyuki
APPLICANT: FUKUDA, Tsunshiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINS-PREE
                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                         FEATURE:
                                                                                                                                                                             MOLECULE TYPE: Synthetic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: M
                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                       ENGTH:
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                                                                                                                                                                                                                                                                                     252 base pairs
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KURIYAMA, Masato
                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
SYSTEM: DOS
                                                                                                                        Synthetic DNA
                                                                   Coding Sequence
1...252
56.6%;
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                                                                                                                                                                                                                                                                                                                              34:
                                                                                                                                                                                                                                                                                                                                                                                                                     41614-FWC
 Score 52.6; DB 2;
Pred. No. 1.4e-08;
                Length 252;
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US-09-108-661-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: NISHIMU
APPLICANT: KURIYAM
APPLICANT: KOYAMA,
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/350,709
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S.
NAME: DAVID, RESNICK S.
                                                                                                                                                                                                                                                             TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO:
            FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGANISM: Synt
FEATURE:
NAME/KEY: Codi
LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                        ANTI-SENSE:
                                                                                                                                     MOLECULE TYPE: S
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                           LENGTH: 252 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCGGAACGUGGAACGUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NISHIMURA, Osamu
KURIYAMA, Masato
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                                                                                                                                                                           linear
                                                                  Synthetic DNA
                  Coding Sequence
1...252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                         Synthetic DNA
                                                                                                                                                                                            double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 6287806uyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/09/108,661
                                                                                                                                                                                                                                                                  34:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                              Post-processing:
Published Applications NA Main:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO8A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

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6: /cgn2_6/ptodata/1/pubpna/USOA_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USOC_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USOC_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USOC_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USOC_PUBCOMB.seq:*
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93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9793542 segs, 4134689005 residues
                                                                                                                                                                                                                                                                                 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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23	21	20	19	18	17	16	15	14	13	12	11	10	9	<b>8</b>	7	6	s	4.	w	2	<b>р</b>	Result No.
57.4	57.4	89	68	89	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	69.6	Score
57.8	61.7	73.1	73.1		74.8		74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	74.8	Query Match Length
106	717	489	489	489	426	420	321	291	291	282	276	276	276	264	252	252	117	111	111	102	102	•
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US-10-848-2/9-6 US-09-746-945-11	US-10-848-279-7	US-10-407-078-43	US-10-407-078-14	US-10-117-109-14	US-10-997-762-20	US-10-997-700-93	US-10-997-700-91	US-10-997-700-77	US-10-997-700-76	US-10-997-078-133	US-10-997-700-75	US-10-997-822-3	US-10-997-762-18	US-10-997-700-89	US-10-997-700-35	US-10-997-078-62	US-10-997-078-141	US-10-997-700-34	US-10-997-078-61	US-10-997-700-33	US-10-997-078-60	ID
Sequence 11, Appl	٦, ٥	Sequence 43, Appl	Sequence 14, Appl	Sequence 14, Appl	Sequence 20, Appl	•	•	Sequence 77, Appl	•		Sequence 75, Appl	~	Sequence 18, Appl	•	Sequence 35, Appl	_	Sequence 141, App		Sequence 61, Appl		Sequence 60, Appl	Description

GENERAL INFORMATION:

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57.8 107 57.6 348 6 57.6 432 6 57.6 432 6 57.6 874 6 56.6 107 6 51.4 102 9 51.4 102 9	45	44	43	42	41	40	39	38	37	36	U U	34	ω G	32	31	0	સ 9	28	27	26	25	24
1407 1407	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	51	52.6	53.6	53.6	53.6	53.6	53.6	53.6	53.8
	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	54.8	56.6	57.6	57.6	57.6	57.6	57.6	57.6	57.8
3 US-09-746-945-12  6 US-10-437-038-1  6 US-10-437-038-3  6 US-10-437-038-7  6 US-10-359-091-7  6 US-10-359-091-7  6 US-10-343-189-15  9 US-10-775-204-24  9 US-10-775-204-51  9 US-10-775-204-60  9 US-10-775-204-61  9 US-10-775-204-63	201	102	102	102	102	102	102	102	102	102	102	102	102	258	102	874	874	432	432	348	348	107
US-09-746-945-12 US-10-437-038-3 US-10-437-038-3 US-10-437-038-3 US-10-359-091-7 US-10-359-091-7 US-10-343-189-15 US-10-775-204-24 US-10-775-204-51 US-10-775-204-61 US-10-775-204-61 US-10-775-204-64 US-10-775-204-1336	ø	9	9	9	φ	<u>ဖ</u>	9	9	9	9	9	9	9	œ	σ	9	σ	σ	σ	9	6	w
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	1386, Ap	1435, Ap	1434, Ap	72, App1	69, App1	64, Appl	61, Appi	60, Appl	57, App1	52, App1	51, Appl	25, Appl	24, App1	15, App1	14, App1	7, Appli	7, Appli	3, Appli	3, Appli	1, Appii	1, Appli	

## ALIGNMENTS

RESULT 1

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US-10-997-078-60
; Sequence 60, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Wagner, E.
; APPLICANT: Holmquist, B.
; APPLICANT: Restoragen, Inc.
; APPLICANT: Restoragen, Inc.
RESULT 2

US-10-997-700-33

: Sequence 33, Application US/10997700

; Publication No. US20050239172A1
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; OTHER INFORMATION: PTH(1-34).
US-10-997-078-60
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627.010US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 102
TYPE: DNA
ORGANISM: Unknown
                                                                                                                                              62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                            62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                              74.8%; Score 69.6; DB 9; 63.0%; Pred. No. 2.6e-15; rative 20; Mismatches 14;
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Sequence 61, Application US/10997078

Publication No. US20050221444A1

GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Magner, F.
APPLICANT: Melonguist, B.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
APPLICANT: NUMBER: US/10/97,078

CURRENT APPLICATION NUMBER: US/10/97,078

CURRENT APPLICATION NUMBER: DOT/US3/16643

PRIOR APPLICATION NUMBER: US 60/383,370

PRIOR APPLICATION UNUMBER: US 60/383,370

PRIOR APPLICATION SUMBER: US 
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US-10-997-078-61
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, OTHER INFORMATION: PTH(1-34).
US-10-997-700-33
                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 58
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APPLICANT: Peng, L.
APPLICANT: Xia, Ut.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REPERBURGE: 1627-009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 102
TYPE: DNA
ORGANISM: Unknown
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Unknown
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62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                              74.8%; Score 69.6; DB 9; ilarity 63.0%; Pred. No. 2.6e-15; Conservative 20; Mismatches 14;
                                                                                                                                                                                                                                                                     74.8%; Score 69.6; DB 9;
larity 63.0%; Pred. No. 2.7e-15;
Conservative 20; Mismatches 14;
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APPLICANT: Holmquist, B.

FIITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
FILE REFERENCE: 1627.009US1
; CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
; PRIOR FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
LENGTH: 111
                                                                                        ; FEATURE:
; OTHER INFORMATION: A synthetic PTH sequence.
US-10-997-078-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 141, Applica
publication No. US200
GENERAL INFORMATION:
APPLICANT: Wagner, F
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; Publication No. US200.
; GENERAL INFORMATION:
APPLICANT: Wagner, F
APPLICANT: Peng, L.
; APPLICANT: Holmquis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-997-700-34
                                                                                                                                                                                                      APPLICANT: Holdquist, B.
APPLICANT: Holdquist, Inc.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
FILE REPERENCE: 1627 0,10161
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR PRILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: N.117
Query Match 74.8
Best Local Similarity 63.0
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                            ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peng, I
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o. US20050221444A1
                                                                                                                                                                  Sequence
  74.8%; Score 69.6; DB 9; 63.0%; Pred. No. 2.7e-15; tive 20; Mismatches 14
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                                            Length 117;
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14;

Indels

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APPLICANT: Xia, U.

APPLICANT: Holmquist, B.

APPLICANT: Holmquist, B.

TITLE OF INVENTION: Methods and DNA Constructs for File Reference: 1627.009US1

CURRENT APPLICATION NUMBER: US/10/997,700

CURRENT FILING DATE: 2004-11-24

PRIOR APPLICATION NUMBER: US/10/997,700

CURRENT FILING DATE: 2002-05-24

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 93

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for FILE REFERENCE: 1627.010US1
CURRENT APPLICATION NUMBER: US/10/997.078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PSI/US/16643
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR TILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOPTWARE: FastSEQ for Windows Version 4.0
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US-10-997-078-62
; OTHER INFORMATION: US-10-997-700-35
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                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/10997700 Publication No. US20050239172A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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                                                                                                 SEQ ID NO 35
LENGTH: 252
                                                                                                                                                                                                                                                                                                                       APPLICANT: Wagner, F. APPLICANT: Peng, L. APPLICANT: Xia, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Holmquist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Unknown
                                      TYPE: DNA
ORGANISM: Unknown
FEATURE:
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                     PTH(1-84)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 69.6; DB 9;
Pred. No. 3.3e-15;
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                                                                                                                                                                                                                                                                                     for High Yield
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                                                                                          APPLICANT: Seo, Jin Seog
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Homquist, Barton
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Polypeptide Cleavage Process
FILE REFERENCE: 1627.026US1
CURRENT APPLICATION NUMBER: US/10/997,762
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16468
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR FILING DATE: 2002-05-24
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
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US-10-997-700-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
TITLE REFERENCE: 1627.009US1
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER: OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 89
LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 89, Application US/10997700
publication No. US20050239172A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
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Best Local S
                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 18 LENGTH: 276
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/10997762 Publication No. US20050227313A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 74.8%;
Best Local Similarity 63.0%;
                                                                             NUMBER OF SEQ ID NOS:
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CUGUTUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCGGAACUCCAUGGAACGUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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63.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69.6; DB 9;
Pred. No. 3.4e-15;
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GENERAL INFORMATION:

APPLICANT: Holmquist, B.

APPLICANT: Holmquist, B.

APPLICANT: Gensalk, X.

APPLICANT: Cryer, R.

APPLICANT: GENSALK, X.

APPLICANT: Cryer, R.

CURRENT FILING DATE: 2004-11-24

PRIOR APPLICATION NUMBER: PCT/US03/16647

PRIOR APPLICATION NUMBER: BCT/US03/16647

PRIOR APPLICATION NUMBER: US 60/383,484

RRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 9

SEQ ID NO 3

LENGTH: 276

TYDE: NOS
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US-10-997-700-75
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7 OTHER INFORMATION: Nucleotide sequence of a
US-10-997-822-3
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US-10-997-822-3
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Sequence 75, Application US/10997700
Publication No. US20050239172A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627,009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 74.8
Best Local Similarity 63.0
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10997822 Publication No. US20050227314A1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                         173 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                           233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                      2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGAACUCCAUGGAACGUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGAAIGGCIGCGIAAAAAACIGCAGGACGIT 264
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63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                         74.8%; Score 69.6; DB 9; 63.0%; Pred. No. 3.4e~15; tive 20; Mismatches 14;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 276;
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US-10-997-078-133
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US-10-997-700-76
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                  Sequence 76, Application
Publication No. US20050;
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Eeng, L.
APPLICANT: Xia, U.
                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 58
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Best Local S
Matches 58
       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                               58;
                                                                                  Application US/10997700
No. US20050239172A1
     Holmquist,
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APPLICANT: Restoragen, Inc.

TITLE OF INVENTION: Methods and DNA Constructs fo: TITLE REFERENCE: 1627.010US1

FILE REFERENCE: 1627.010US1

CURRENT APPLICATION NUMBER: US/10/997.078

CURRENT FILING DATE: 2004-11-24

PRIOR APPLICATION NUMBER: PCT/US03/16643

PRIOR FILING DATE: 2003-05-23

PRIOR FILING DATE: 2003-05-23

PRIOR PRIOR APPLICATION NUMBER: US 60/383,370

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 148

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 133

LENGTH: 282
                                                                                                                                                                                                        ; OTHER INFORMATION: A US-10-997-078-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: A US-10-997-700-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 133, Application US/10997078
Publication No. US20050221444A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Yie, U.
APPLICANT: Xie, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 93
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75
LENGTH: 276
                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                  227 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 258
                  62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93 ::|||:|||:|||:||||||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 105
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                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                       74.8%; Score 69.6; DB 9; 63.0%; Pred. No. 3.4e-15; tive 20; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.8%; Score 69.6; DB 9; 63.0%; Pred. No. 3.4e-15; cive 20; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR
                                                                                                                                                                                                                                 sequence for the T7tagVg-PTH(1-34)
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                                                                                                                                                                            Length 282;
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APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for FILE REFERENCE: 1.627.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
LENGTH: 291
                                                                         RESULT 15
US-10-997-700-91
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US-10-997-700-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 76
LENGTH: 291
TYPE: DNA
                    Sequence 91, Application US/10997700 Publication No. US20050239172A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 77, Application US/10997700 Publication No. US20050239172A1
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627.009US1 CURRENT APPLICATION NUMBER: US/10/997,700 CURRENT FILING DATE: 2004-11-24 PRIOR APPLICATION NUMBER: US 60/383,212 PRIOR FILING DATE: 2002-05-24 NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wagner, F. APPLICANT: Peng, L. APPLICANT: Xia, U.
APPLICANT: Wagner, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: A synthetic PCR product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                          89
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::|||:|||:|||:|||||||:|||||||::
89 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 120
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                                                                                                                                                                                               62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                  58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCGGAACUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                           2 CUGUTUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                          TTGAATGGCTGCGTAAAAACTGCAGGACGTT 120
                                                                                                                                                                                                                                      CTGTTTCTGAAATCCAGCTGATGCACAACCTGGTAAACACCTGAACTCTATGGAACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                74.8%; Score 69.6; DB 9; 63.0%; Pred. No. 3.4e-15; tive 20; Mismatches 14;
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Pred. No. 3.4e-15;
20; Mismatches 14;
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; FEATURE:
; OTHER INFORMATION: A synthetic pBN121-T7tag-CH-PTH(1-84).
US-10-997-700-91
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APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic FILE REFERENCE: 1627.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91
TENGTH: 321
                                                                                                                                                                             Matches
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Best Local Similarity
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122
                         62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                     62 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
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TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 153
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Pred. No. 3.5e-15;
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2005 Compugen Ltd.
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 US-11-167-273-2
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US-10-526-731-4
US-11-184-005-23
US-10-131-826A-351
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US-11-074-176-353
US-11-074-176-353
US-11-074-176-185
US-10-793-626-4301
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US-10-980-459-27
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Matches Qy Db 1		RESULT 1 US-11-167- ; Sequence ; Publicat ; GENERAL ; APPLICA ; APPLICA ; APPLICA ; APPLICA ; APPLICA ; APPLICA	ט ט פ. פ. פ. פ. פ.	0 0 0 10 0 0 10 0 0 0 10 0 0 0 0	C 25 C 27 28 30
36 15 1122 1122 75	APPLICANT: FILIPP APPLICANT: FILIPP APPLICANT: CHUDAK TITLE OF INVENTION FILE REFERENCE: 23 CURRENT APPLICATION CURRENT FILING DATE PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR FILING DATE: NUMBER OF SEQ ID NO 2 LENGTH: 1410 TYPE: DNA SOFTWARE: Patentin NEQ ID NA SOFTWARE: Patentin CRGANISM: Escheri-11-167-273-2 Query Match	273- 273- 2, ion ion INFC NT: NT: NT:	20000000000000000000000000000000000000	4 4 4 4 C C	00000000000000000000000000000000000000
36; CONSERVAT  5 CCAGCUGAUGCA                  2 CCTGCTGATGGC 5 UAAAAAAACUGCA	PA, OV, OV, OV, OV, OV, OV, OV, OV, OV, OV	X X B 65		1 1 0 0 0 0 1	# # # # # # # # # # # # # # # # # # #
CONSETVATIVE CCAGCUGAUGCACGGUGG         :                     CCTGCTGATGGCCGGTCT UAAAAAACUGCAGGACGU	Tria Getri) Tria UTAI UTAI UTAI 1 - 3(1) 1 - 3(1) 1 - 3(1) 1 - 3(1)	A  Application US/11167273 No. US20050255567A1 RMATION: GUSYATINER, Mikhail Mar IVANOVA, Tatyana Vikto MUKHANOVA, Ekaterina I	1606 1 1606 1 15412 1 10439 1 1809 8 1542 1 1929 1 3719 1		636 1 1910 1 11337 1 7893 7 8106 7 23907 7
10; Mism suggueguege :  :  : rTGATGGTAT J 92	Yulia Georgievna Dmitriy Vladmirovich Law Moria Aleksandrovna Ew MOTANT GLUTAMINE S 2005.06-28 UMBER: US/11/167,273 2005-06-28 1005.11-20 101132473 101-11-30 105.5 28.88; Score 26.8; 28.88; Score 26.8;	ALIGNMENTS on US/11167273 5025567A1 R. Mikhail Markovich AYA, Lirina Valerievna Tatyana Viktorovna A, Ekaterina Igorevna	US-10-131- US-10-131- US-10-231- US-10-931- US-11-132- US-11-132- US-10-990- US-10-131- US-10-131-	US-11-03 US-10-82 US-10-82 US-10-82 US-10-85	US-10-980 US-10-821 US-10-499 US-11-186 US-11-186 US-11-186
AGP	vladmirovich Aleksandrovna T GLUTAMINE SYNTHETASE VT GLUTAMINE SYNTHETASE Syll/167,273 Syll/299,799 Coolise 2473 Coolise 26.8; DB 7; I Pred. No. 0.79;	MENTS  Ch  evna  a  na	1-826A-65 1-826A-257 1-834-36 3-509-1 2-839-6 0-276-4 1-234-50 1-236A-49	11-13-764-19 -11-033-764-19 -10-821-234-83 -10-821-234-277 -11-150-406-1 -10-821-234-290 -10-828-730-53	0-459-8 9-734-211 9-715-1 6-731-3 6-731-6 6-731-6
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Gaps 0; CUGCG 74 :  CATGGA 1181	PRODUCING		65, Appl 257, App 36, Appl 1, Appli 6, Appli 4, Appli 50, Appl	19, Appl 83, Appl 277, Appl 1, Appli 290, Appl	8, Appil 211, Appil 1, Appil 3, Appil 1, Appil 1, Appil 1, Appil 6, Appil

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RESULT 2 US-10-821-234-760/c ; Sequence 760, Application US/10821234 ; Publication No. US20050255114A1 ; GENERAL INFORMATION:

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US-11-184-005-23/c

| Sequence 23, Application US/11184005
| Publication No. US20050256052A1
| GENERAL INFORMATION:
| APPLICANT: Luyten, Frank P.
| APPLICANT: Moos, Malcolm JR.
| APPLICANT: Hoang, Bang
| APPLICANT: Hoang, Bang
| APPLICANT: Wang, Shouwen
| TITLE OF INVENTION: METHOD OF MODULATING TISSUE
| TITLE OF INVENTION: GROWTH USING FRZE PROTEIN
| FILE REFERENCE: NITH133.1CPC3
| CURRENT APPLICATION NUMBER: US/11/184,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10526731

| Publication No. US20050244437A1
| GENERAL INFORMATION: |
| APPLICANT: AKZO NObel N.V. |
| TITLE OF INVENTION: live attenuated parasite vace |
| FILE REFERENCE: 2002-017-EP |
| CURRENT APPLICATION NUMBER: US/10/526,731 |
| CURRENT APPLICATION NUMBER: BP 02078953 |
| PRIOR APPLICATION NUMBER: EP 02078953 |
| PRIOR FILING DATE: 2002-09-20 |
| NUMBER OF SEG ID NOS: 29 |
| SOFTWARE: PatentIn version 3.2 |
| SEG ID NO 4 |
| LENGTH: 2748 |
| TYPE: DNA |
| ORGANISM: Toxoplasma gondii |
| US-10-526-731-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 760
SEQ ID NO 760
TYPE: DNA
NRANLISM: Homo sapiens
US-10-821-234-760
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US-10-526-731-4
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TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Labat, Ivan
APPLICANT: Stache-Cra:
APPLICANT: Andarmani,
APPLICANT: Tang, Y. To
                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                     38 GUGGUCUGAACUCCAUGGAACGUGUUGAAAUGGCUGCGUAAAAAACUGC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 AAAAAACUGCAGGACGUU 93
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nilarity 54.2%;
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Conservative 1:
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                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 1; Length 2748; Pred. No. 9.3; 7; Mismatches 15; Indels
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: D3330R1C128
FILE REFERENCE: D3330R1C128
CURRENT APPLICATION UNMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/05913
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PRIOR PRIOR DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/05912
PRIOR APPLICATION NUMBER: 60/05913
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059263
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PRIOR APPLICATION NUMBER: US 10/028051
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 08/822333
PRIOR FILING DATE: 1997-03-20
PRIOR APPLICATION NUMBER: US 08/729,452
PRIOR FILING DATE: 1996-10-11
NUMBER: OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 1291
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Sequence 351, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION
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; ORGANISM: Xenopus laevis
US-11-184-005-23
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FILING DATE:
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Similarity 40.4%; Pred. No. 13;
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Wood, William
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Gerritsen, Mary E
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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DeForge, Laura
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US-10-510-386-67

US-10-10-386-67

; Sequence 67, Application US/10510386

; Publication No. US20050244922A1
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                                                                                                                                   Sequence 35, Application US/11033764
Publication No. US20050244817A1
GENERAL INFORMATION:
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APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: Patentin version 3.3
SEQ ID NO 67
SEQ ID NO 67
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LENGTH: 4053
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APPLICANT: Clausen, Ib Groth
APPLICANT: Jorgensen, Steen Troels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/059588 PRIOR FILING DATE: 1997-09-19
APPLICANT: Rubin, Donald H.
APPLICANT: Organ, Edward L.
APPLICANT: DuBois, Raymond N.
TITLE OF INVENTION: Mammalian Genes Involved in Viral
TITLE OF INVENTION: Infection and Tumor Suppression
FILE REFERENCE: 01123.0004
CURRENT APPLICATION NUMBER: US/11/033,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2206
TYPE: DNA
ORGANISM: Bacillus licheniformis
FEATURE:
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LOCATION: (501)..(1703)
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                                                                                                                                                                                                                                                                                   619 TTAAAAACAGGCCG 632
                                                                                                                                                                                                                                                                                                                                                                559 TCTGCCTGATGATTGAAGCGGGTGCGGGAATGAACACGACTGAACAGTTTGAGAGCTTAT 618
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                                                                                                                                                                                                                                                                                                                                                                                                     14 UCCAGCUGAUGCACGGUGGUGGUGGUGUGGAACUCCAUGGAACGUGUUGAAUGGCUGC
                                                                                                                                                                                                                                                                                                                        74 GUAAAAAACUGCAG
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33; Conserv
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40.5%; Pred. No. 20;
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Pred. No. 24
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Mismatches
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PRIOR APPLICATION NUMBER: US/10/877,807
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/509,712
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US98/21276
PRIOR APPLICATION NUMBER: PCT/US98/21276
PRIOR FILING DATE: 1998-10-08
PRIOR PFLICATION NUMBER: 60/062,021
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 127
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                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-10-821-234-224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 224, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y Tom
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SEQ ID NO 35
LENGTH: 320
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                                                                                                                                                                                                                                                                                                         SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 224
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Best Local Similarity
                                                                                                                                                     Matches
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: 1- 320
OTHER INFORMATION: n = 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                 LENGTH: 11438
TYPE: DNA
                                                                                                                                                 / Match 24.1%;
Local Similarity 47.2%;
nes 34; Conservative
3946 AGAAGGTCTGCA 3957
                                                                         3886 CCAGCTGCTGTGCGTGGGCCTCCGCCACTAGACGCAGCTTGCTGCCCGCCGGGG 3945
                                                                                                           15 CCAGCUGAUGCACGGUGGUGGUGGUCUGAACUCCAUGGAACGUGUUGAAUGGCUGCG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 AACCAGIGTATACTCTGCCATGGTCCAGGCCTGTACTTCTGTGATCTTGTGTCATGGGTG 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 ÇGUA 76
                                   75 UAAAAAAÇUĞÇA 86
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Pred. No. 20;
10; Mismatches
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                                                                                                                                                     7;
                                                                                                                                                                       Score 22.4;
Pred. No. 51;
                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of Preeclampsia
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                                                                                                                                                                                         Length 11438;
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RESULT 9 US-11-082-389-315

; Sequence 315, Application US/11082389

Publication No. US20050244935A1

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APPLICANT: Zelger, USKAI
APPLICANT: Haberhauer, Gregor
ITILE OF INVENTION: CORYNBEACTBRIUM GLUTAMICUM GENES ENCODING PROTEINS
ITITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
ITITLE OF INVENTION: TRANSPORT
IFLE REFERENCE: BGI-131CPCN
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR APPLICATION NUMBER: UB 19930489.0
PRIOR APPLICATION NUMBER: UB 19930489.0
PRIOR APPLICATION NUMBER: UB 19931549.3
PRIOR APPLICATION NUMBER: UB 19931549.3
PRIOR APPLICATION NUMBER: UB 19931550.7
PRIOR APPLICATION NUMBER: UB 19931550.7
PRIOR APPLICATION NUMBER: UB 19931550.7
PRIOR APPLICATION NUMBER: UB 19931549.3
PRIOR APPLICATION NUMBER: UB 19931549.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: UB 19931550.7
PRIOR APPLICATION NUM
GENERAL INFORMATION

APPLICANT: Klaenhammer, Todd R.

APPLICANT: Russell, William M.

APPLICANT: Altermann, Eric

APPLICANT: Altermann, Eric

APPLICANT: McAuliffe, Olivia

TITLE OF INVENTION: Nucleic Acid Sequences Encoding

TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore

FILE REFERENCE: 5051-694

CURRENT APPLICATION NUMBER: US/11/074,176

CURRENT APPLICATION NUMBER: 60/551,161

PRIOR APPLICATION NUMBER: 60/551,161

PRIOR APPLICATION STRESS AND NOW STRESS APPLICATION OF SERVICE STRESS APPLICATION NUMBER: 60/551,161

PRIOR PLING DATE: 2006-03-08

NUMBER OF SEG ID NOS: 381

NUMBER OF SEG ID NOS: 381
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US-11-074-176-353
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEATURE:
NAME/KEY: CDS
LOCATION: (101)...(1438)
OTHER INFORMATION: RXN01995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1148 GTTGTGGGCATGCTGATCAATGGTTGTGTGGCTGGTCTGTACACCCTG 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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Zelder, Oskar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/11074176
5. US20050250135A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.9%; Score 22.2; ilarity 45.1%; Pred. No. 35; Conservative 10; Mismatches
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PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 185
LENGTH: 1224
TYPE: DNA
ORGANISM: Lactobacillus acidophilus
FEATURE:
FEATURE: CC6
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US-11-074-176-185
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; NAME/KEY: misc feature
; LOCATION: (0): ...(0)
; OTHER INFORMATION: ORF 699; phosphoglycerate kinase
US-11-074-176-353
                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 699; phosphoglycerate kinase
US-11-074-176-185
                                                                                                                                                                    US-10-793-626-4301/c
                                                                                                                                                                                       RESULT 12
Sequence 4301, Application US/10793626
publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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Best Local
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APPLICANT: McAuliffe, Olivia
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Klaenhammer, Todd R. APPLICANT: Russell, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE: misc_feature
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Lactobacillus acidophilus
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NAME/KEY: CDS
LOCATION: (1)...(1209)
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                                                                                                                                                                                                                                                                                         28 GGUGGUGGUGGUGUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUA 76
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(1)...(1224)
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Pred. No. 4
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PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1

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; OTHER INFORMATION: Description of Artificial Sequence: synthetic ; OTHER INFORMATION: nucleic acid sequence US-10-793-626-4301
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-748
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and
FILE REFERENCE: 821A
FULE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 112, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: pt_SEQ_genes Version 1.0 SEQ ID NO 748
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Best Local :
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CURRENT FILLING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
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APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2536
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 23.2%; Score 21.6; DB 1; Length 1759;
Local Similarity 44.1%; Pred. No. 60;
nes 30; Conservative 9; Mismatches 29; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1705 TGGTTTTGGTTTCTACTCCAAGAAAGGAATAGCATGACTGATTATGAAA 1657
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SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 112
LENGTH: 3901
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
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New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.

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                                                                                                                                                                                    (GARD/)
(KRON/)
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                                                                                                                                  Kronenberg
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                                                                                                                                                                                                                                                                                                                                                                              99WO-US031108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .93
/*tag= a
/product= "PG5"
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                                                                                                                                  Ĭ,
amino terminal signaling functional domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 93; DB 3; L
Pred. No. 3.7e-20;
                                                                                                                                     Potts
                                                                                                                                  JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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linked to a carboxy-terminal binding portion of parathyroid treating mammalian conditions characterized by decreases in
                                                                                                         Claim 14;
                                                                                                        Fig 1; 119pp; English.
                                                                                                                       hormone for bone mass.
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Compounds of the structure or formula S-(L)\_n-B, R-1-S-(L)\_n-R or S-(L)\_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PPH), L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PPH(1-34) or a PTH-related protein (PPH-rP) (1-34); R 1 is the sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis

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                                                                                                     Query Match
                                                                                                                          Sequence
61
                 61
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                                                                                  87;
                                                                                            Similarity
                                                     GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU
GUUGAAUGGCUGCGUAAAAACUGCAGGACGUU
              GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
                                       GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUCUGAACUCCAUGGAACGU
                                                                                                                          93 BP; 21 A; 18 C; 30 G; 0 T; 24 U; 0 Other;
                                                                                  Conservative
                                                                                          89.7%;
                                                                                  Score 83.4; D
Pred. No. 4.6e
0; Mismatches
                                                                                  0
                                                                                            DB 3; Length 93; .6e-17;
                   93
 93
                                                                                  0;
                                                                                  Gaps
                                           60
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RESULT 3
AAA5171
ID AAA5
XX AAA517
XX AAA5
XX AAA5
XX PTH
XX PTH
XX PTH
XX HOMO
OS Syntt
XX HOMO
OS Synt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTH; parathyroid hormone; conjugate; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTH functional domain conjugate peptide PG9 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA51731 standard; RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Homo sapiens.
Synthetic.
                      Location/Qualifiers
1. .93
/*tag= a
/product= "PG9"
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WO200039278-A2
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30-DEC-1999; 06-JUL-2000. 99WO-US031108

31-DEC-1998; 98US-0114577P

(GARD/) GARDELLA T J. (KRON/) KRONENBERG H M. (POTT/) POTTS J T. (JUEP/) JUEPPNER H.

WPI; 2000-452384/39 P-PSDB; AAY96974. Gardella TJ, Kronenberg Ĭ, Potts JT, Jueppner Ξ

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ART73910 1
AAT73910 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein; recombinant production; endoproteinase LysC; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic oligonucleotide encoding linker and PTH 1-37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
30-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT73910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Fig 1; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT73910 standard; DNA; 152 BP.
                                                                                           16-NOV-1995;
                                                                                                                                                   06-NOV-1996;
                                                                                                                                                                                                               22-MAY-1997.
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                                  (BOEF )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ب
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                                  BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGU 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 18 A; 14 C; 35 G; 0 T; 26 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                        95DE-01042702.
                                                                                                                                                       96WO-EP004850
                                                                                                                                                                                                                                                                                                                                    /*tag= b
/*tag= b
/label= sticky_end
/note= "5' end of complementary strand overhangs 3'
of present strand by sequence 5'-TCGA-3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64.2; DB 3; Pred. No. 7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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ADG93179
ADG93179
ADG93179
ADG93179
AC ADG9
XX ADG9
XX ADG9
XX ADG9
XX Hove
XX Hov
XX Hov
XX Hov
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XX Hov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence, which encodes a linker and the parathyroid hormone CC 1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was CC ligated to the 2.9 kb Nhel-HindIII fragment of pSAM-CORE, which contains CC the Met(13-139) streptavidin (SA) sequence, to give pSA-EK-PTH. pSA-EK-CC PTH and the LacIq repressor plasmid pUBS500 were used to transform E. CC coli K12 RM82. The transformants were grown, with IPTG induction, in CC medium containing kanamycin and amplicilin. Cells were harvested, lysed CC and isolated inclusion bodies solubilised in guanidine hydrochloride, and CC renatured by dilution in pH 7 phosphate buffer. The solution was CC clarified and the supernatant concentrated and purified on a column of CC immobilised iminobiotin. The purified material was incubated with CC endoproteinase LysC and the PTH 1-37 fragment released, recovered by SA CC fragment removal on an iminobiotin column followed by chromatography on a CC fractogel and reverse phase HPLC. The endoproteinase LysC cleaves the CC fusion protein rapidly and completely, exclusively at the Lys residue in CC the linker, i.e. nor ** Iva residue** in SA (Indated on 35.MM2-2001 **).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant production of peptide(s) as fusions with streptavidin attached via cleavable linker - especially for urotropin and parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 2; 37pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hormone production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW21946
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WPI; 2004-035128/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression cassette; high yield polypeptide production tandem polypeptide; inclusion body; gene; ds.
                                                                Harley S,
                                                                                                                                                                                                                                                                                               23-MAY-2003; 2003WO-US016643
                                                                                                                                                                                                                                                                                                                                                        04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003100021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel expression cassette-related polypeptide-encoding DNA SeqID60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG93179 standard; DNA; 102 BP
                                                                                                                                (REST-) RESTORAGEN INC. (HARL/) HARLEY S.
                                                                                                                                                                                                                               24-MAY-2002; 2002US-0383370F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGTTTCCGAAATCCAGCTGATGCACACCTGGGTAAACACCTGAACTCCATGGAACGTG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 128
                                                                Williams JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not at Lys residues in SA. (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.2%;
                                                                Luan P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 61.6;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                   Xia Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; DB 2;
5.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
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RESULTS
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Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
                                                                                                                                                                                           New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
                                                                                                                                            Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-2002; 2002US-0383212P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-2003; 2003WO-US016645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTH peptide coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 60; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REST-)
                                                                                                                                                                                                                                                                                                                2004-035129/03
DB; ADJ65837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 TIGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                     33; 132pp;
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Pred. No. 1.6e-09;
9; Mismatches 20;
                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
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The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide polypeptide in a cell, preferably a tandem polypeptide that forms an

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UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93

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                                                                                                 Query Match
Best Local S
Matches 53
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Best Local S
Matches 53
                                                                                                                                                                                                                               The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PrH 1-34 peptide (ADW14376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and separating by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the PTH 1-34 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inclusion body when expressed in a a peptide which may be used in the of the invention.
                                                                                                                                                                                          Sequence 102 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of reorganized human parathyroid hormone 1-34 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-2001; 2001CN-00142627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2004-099606/11.
DB; ADW14378.
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53; Conserv
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53; Conser
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          UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||::
TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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                                                                                              64.5%;
larity 57.6%;
Conservative 1
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                                                                                                                                                                                       30 A; 24 C; 22 G;
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57.6%;
                                                                                                                                                                                                                                                                                                                                                                                            3; 25pp; Chinese.
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                                                                                                   19;
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                                                                                              Score 60; DB
Pred. No. 1.6e
19; Mismatches
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Pred. No. 1.6e
19; Mismatches
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                                                                                                                                                                                          26 T; 0 U; 0 Other;
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                                                                                                                                                DB 13;
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                                                                                                   ..6e-09;
les 20;
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les 20;
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                                                                                                                                           Length 102;
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RESULT 8
ADG93180
RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harley S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression cassette; high yield polypeptide production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel expression cassette-related polypeptide-encoding DNA SeqID61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 61; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
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                                       06-MAY-2004
                                                                                          ADJ65858 standard; DNA; 111 BP
                                                                                                                                                                                                                                                                                                                Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;
          peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide; inclusion body; gene; ds.
                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESTORAGEN INC
                                                                                                                                                                         UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                       CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGAACGUG
                                                                                                                                                                                                           CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
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             coding
                                                                                                                                                                                                                                                               Conservative
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                                       (first entry)
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             sequence #2
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57.6%;
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Pred. No.
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                                                                                                                                                                                                                                                                            1.6e-09;
                                                                                                                                                                                                                                                                                        DB 12;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a peptide which may be used in the construction of a tandem polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression cassette; tandem polypeptide; inclusion body; inclusion body, fusion partner; PTH; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New expression cassette comprising an operably linked nucleic sequence, useful for producing a tandem polypeptide that forms inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2003; 2003WO-US016645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 34; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-035129/03.
P-PSDB; ADJ65838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-2002; 2002US-0383212P
                                                                                                                                                                                    Human parathyroxin Gly-Ser-Pro-PTH 1-34 peptide DNA SEQ ID
                                                                                                                                                                                                              10-MAR-2005
                                                                                                                                                                                                                                                              ADW14375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 111 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REST-) RESTORAGEN
                                    12-DEC-2001; 2001CN-00142627.
                                                           12-DEC-2001; 2001CN-00142627
                                                                                                                                    Homo sapiens
                                                                                    18-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                             parathyroxin;
                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                    62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
                                                                                                                                                                                                                                                                                                                                                                                                                             53;
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                                                                                                                                                                                                                                                                                                                                                                             CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                    cugurucceaaanuccaecueauecaceeueeueeueeueeueeueeuuccaueeaaceue
                                                                                                                                                                                                                                                                                                                            TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
                                                                                                                                                                                                                                                              standard; DNA; 111 BP
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 A; 26 C;
                                                                                                                                                              recombinant protein; protein engineering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                        57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB 12, Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 G; 30 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 111,
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(SHAN-) SHANGHAI BIOLOGICAL ENG

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RESULT 11
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the Gly-Ser-Pro-PTH 1-34 peptide.
                                                            New expression cassette comprising an operably linked nucleic a sequence, useful for producing a tandem polypeptide that forms inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen
                                                                                                                                                                                                               04-DEC-2003
                                                                                                                                                                                                                                                                            expression cassette;
tandem polypeptide;
                                                                                                                                                                                                                                                                                                                                                              ADG93260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ
                                             Disclosure;
                                                                                                                              Harley
                                                                                                                                                                           24-MAY-2002; 2002US-0383370P
                                                                                                                                                                                             23-MAY-2003; 2003WO-US016643
                                                                                                                                                                                                                                 WO2003100021-A2
                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                        Novel expression cassette-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 111 BP; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of reorganized human parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                   2004-035128/03
DB; ADG93259.
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DB; ADW14376.
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                                                                                                                                                RESTORAGEN INC
HARLEY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                           TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 102
                                                                                                                                                                                                                                                                                                                                                                                                                     UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
                                                                                                                                                                                                                                                                                                                                                                                                                                               CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUGCACGGAACGUG
                                                                                                                              Williams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                             IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO 1; 25pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŀi
                                           NO 141; 157pp;
                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 28 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                            high yield polypeptide production; inclusion body; gene; ds; PTH.
                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.6%;
                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                               Luan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 G; 27
                                                                                                                              ָיש
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                           English.
                                                                                                                                                                                                                                                                                                         PTH DNA SeqID141
                                                                                                                               Xia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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This invention relates to a novel expression cassette and methods high yield production of polypeptides. The cassette comprises an oplinked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expression of the case to produce a tandem polypeptide that forms an inclusion body when expression of the case to the case the case to the case 
expressed operably 101

Sequence

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Other;

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AAT34865
ID AAT34
ACC
XX AAT34
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XX P1ASM
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KW PTH;
KW Vecto
OS Synth
XX VSPH
KW Vecto
OS Synth
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Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                    and transpeptidation of r constructs.
                                              A portion (AAT34865) of plasmid pBN1:PTH(1-34)C-1c comprises DNA coding for a fusion protein (AAR87867) composed of the C-terminal end of human carbonic anhydrase II joined by an intraconnecting peptide (including a thrombin cleavage site) to amino acids 1-34 of PTH (AAR98866), followed by a Cys residue and C-terminal sequence. The complete construct can be expressed in E. coli transformants. The intraconnecting peptide and C-terminal Cys residue enable the recombinant protein construct to be selectively reacted to produce C-terminal carboxamidated PTH(1-34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in a cell. The expression cassette is useful for producing peptide polypeptide in a cell, preferably a tandem polypeptide that forms inclusion body when expressed in a cell. The present sequence is the a DNA sequence which encodes a PTH peptide which was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTH; parathyroid hormone; parathormone; alpha-carboxamide; recombinant protein; vector; plasmid pBN1; carbonic anhydrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1994;
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                                                                                                                                                                                                                                                                Example 7; Fig 1; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BION-)
                                                                                                                                                                                                                                                                                                                                                                                                                  PSDB; AAR98967
                                                                                                                                                                                                                                                                                                                                                                                                                                     1996-287185/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patridge
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1. .162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "hCA-linker-PTH(1-34)Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE,
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                                                                                                                                                                                                                                                                                                                                       l alpha-carboxamidated recombinant multicopy
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%; Pred. No. 1.76
19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holmquist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-amide; C-amidated peptide;
fusion protein; transpeptidation;
e II; ss.
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r fusion
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                                                                                                                                                                                This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
                                                                                                                                                                                                                                                                                                                                                       New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression cassette; tandem polypeptide;
                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 62; 157pp; English.
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                                                                                                                                                        Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-035128/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harley S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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                                                                                                               ocal Similarity
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62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93 ::|||:|||:|||:|||:::
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HARLEY S.
                                                                                                                                                                                                                                                                                                                                                                                                                    ADG93161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 138
                                                           CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG
                                            CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams
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                                                                                                             64.5%;
57.6%;
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57.6%;
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; Pred. No. 1.8e-09;
19; Mismatches 20
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Thes 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ65859
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                                                                                          Tandem polypeptide-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 252 BP; 68 A; 65 C; 61 G; 58 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2003.
    expression cassette; tandem polypeptide; inclusion body;
                                                                                                                                                                                06-MAY-2004
                                                                                                                                                                                                                                                                      ADJ65913
                                                                                                                                                                                                                                                                                                                                                   ADJ65913 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 35; 132pp; English.
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les 53; Conserv
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                                                                                          expression cassette #6
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Pred. No.
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Search completed: November 23, 2005, 23:00:14 Job time : 242.667 secs
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                                                                                                                                                                                                                                                         The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence represents an expression cassette which encodes a tandem polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                  New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
                                                                                                                                                                                                                           Sequence 264 BP; 72 A; 67 C; 64 G; 61 T; 0 U; 0 Other;
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P-PSDB; ADJ65912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Хiа Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2002; 2002US-0383212P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REST-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inclusion body fusion partner;
                                                        62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:|||||||::
65 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 96
                                                                                                             ch 64.5%; Score 60; DB 12; Length 264; I Similarity 57.6%; Pred. No. 2e-09; 53; Conservative 19; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peng L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESTORAGEN INC.
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Maximum DB seq length: 200000000
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AR027050	BD170198	BD170211	BD170213	BD170222	BD170195	AR135774	A79761	AR043802	I83596	E05672	AR027021	S71759	I83595	E05671	E04335	AR027020	I83594	E05673	E05658	AR168173	AR030635	AR027044	AR027011	E05675	AR027046	BD234389
AR027050 Sequence		BD170211 Process f	BD170213 Process f	BD170222 Process f	BD170195 Process f	AR135774 Sequence	A79761 Sequence 9	AR043802 Sequence	I83596 Sequence 4	E05672 DNA encodin	AR027021 Sequence	S71759 human parat	I83595 Sequence 3	E05671 DNA encodin	E04335 Synthetic D		I83594 Sequence 1	E05673 DNA encodin	E05658 DNA encodin	AR168173 Sequence	AR030635 Sequence		AR027011 Sequence	E05675 DNA encodin	AR027046 Sequence	BD234389 Recombina

## ALIGNMENTS

Query Match	FEATURES SOURCE ORIGIN			JOURNAL COMMENT	VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 1 BD266833 LOCUS DEFINITION
100.0%; Score 93; DB 6; Length 93;	FT Location/Qualifiers  193 /organism="synthetic construct" /mol_type="genomic RNA" /db_xref="taxon:32630"	C12N15/09, A61R38/ A61P19/10, A61P43/00, C07K14, C12N1/21, C12N5/10, G01N33/1 scription of Artific bocation/Q	PD 08-0CT-2002  PD 08-0CT-2002  PF 30-DEC-1999 JP 2000591171  PR 31-DEC-1998 US 60/114577  PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI JUEEPNER	PTH functional domain conjugate peptides, delivatives thereof and novel tethered ligand-receptor molecules Patent: JP 2002533115-A 2 08-OCT-2002; THE GENERAL HOSPITAL CORP OS Artificial Sequence THE OCCESSION OF THE PROPERTY OF THE PROPER	BD266833.1 GI:33076601 BD266833.1 GI:33076601 JP 2002533115-A/2. synthetic construct synthetic construct other sequences, artificial sequences. 1 (bases 1 to 93) 1 (bases 1 to 93) 1 (bases 1, Kronenberg, H.M., Potts, J.T. and Jueppner, H. Gardella, T.J., Kronenberg, H.M., Potts, J.T. and Jueppner, H.	BD266833 93 bp RNA linear PAT 17-JUL-2003 PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.

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Patent: up 2002533115-A 1 08-OCT-2002;
INT OS Artificial Sequence PN JP 200253115-A/1
PD 08-OCT-2002
PF 30-DEC-1909 JP 2007
PR 31-DEC-1007
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PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N1/21,
PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC PC C12N5/10,G1N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC Description of Artificial Sequence: modified PTH sequence FH Key Location/Qualifiers
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                                                  BD266834 93 bp RNA linear PAT 17-UUL-2003 PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.
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93 bp RNA
PTH functional domain conjugate peptides,
novel tethered ligand-receptor molecules.
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/mol_type="genomic RNA"
/db_xref="taxon:32630"
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SM synthetic construct

other sequences, artificial sequences.

1 (bases 1 to 93)

S 1 (bases 1 to 93)

S Gardella, T.J., Kronenberg, H.M., Potts, J.T. and Jueppner, H.

PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules

novel tethered ligand-receptor molecules

THE GENERAL HOSPITAL CORP

OS Artificial Sequence
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PD 08-OCT-2002

PN J-DEC-1998 US 60/114577

PR 31-DEC-1998 US 60/114577

PR 31-DEC-1998 US 60/114577

PTETENNER MARALD PI

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C12N
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Jung,E.-K., Park,D.-H. and Chung,S.-I.
Jung,E.-K., park,D.-H. and Chung,S.-I.
Recombinant expression vector of human parathyroid hormone
Patent: US 6500647-A 26 31-DEC-2002;
Mogam Biotechnology Research Institute; Kyonggi-Do;
KRX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR269042
Sequence 26 from patent
AR269042
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown.
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                                                                                                    Similarity
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|::|||:|||:||:|||:|||||||::
GTTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC
                                                                             Conservative
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Location/Qualifiers
1. .93
                                                                                                                                                                                                                                                 Location/Qualifiers
1. .258
                                                                                                                                                                                            /organism="unknown"
/mol_type="genomic DNA"
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/mol_type="genomic RNA"
/db_xref="taxon:32630"
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                                                                           61.1%; Score 56.8; DB 6; 54.3%; Pred. No. 3.2e-06; tive 20; Mismatches 22;
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US 6500647.
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AR005132
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AR005133/c
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Matches 51
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Matches
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TITLE
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Sequence 5
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                                                                                                                                                                     Holladay, L.A. and Oldenburg, K.R. Method for increasing the electrotransport Patent: US 5747453-A 5 05-MAY-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 141)
Holladay, L.A. and Oldenburg, K.R.
Method for increasing the electrotransport
Patent: US 5747453-A 3 05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
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                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG
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                                        TTGAATGGCTGCGTAAAAAACTGCAGGATGTT
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                   uugaaugecueceuaaaaaacuecaeeaceu 92
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/mol_type="unassigned
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/mol_type="unassigned
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Pred. No. 1.9e-05;
L7; Mismatches 23;
                                                                                 Score 54.2; DB 6;
Pred. No. 1.9e-05;
7; Mismatches 23;
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RESULT 7
AR177779
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AUTHORS
TITLE
JOURNAL
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ORGANISM
        RESULT 9
AR043797
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AR177780/c
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KEYWORDS
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AR177779
AR177779.1
        Sequence 8 :
AR043797
AR043797.1
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                                                                                                                                                                                                                                                          Unclassified.

1 (bases 1 to 141)

1 (bases 1 to 141)

Holladay, L.A. and Oldenburg, K.R.

Method for increasing the electrotransport

Method for increasing the NOV-2001;

Patent: US 6313092-A 5 06-NOV-2001;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  Unknown.
Unknown.
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AR177780
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Holladay, L.A. and Oldenburg, K.R.
Holladay, L.A. and Oldenburg, K.R.
Method for increasing the electrotransport flux of polypeptides
Patent: US 6313992-A 3 06-NOV-2001;
Location/Qualifiers
                                                                                                                                                                                51;
                                                                                                                                                          2 CUGUTUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGAACGUG 61
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Unclassified.
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/mol_type="unassigned
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                              patent US
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Pred. No. 1.9e-
17; Mismatches
                                                                                                                                                                               Score 54.2; DB 6;
Pred. No. 1.9e-05;
7; Mismatches 23;
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S 6313092.
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5 5814603.
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1.9e-05;
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PAT 05-MAR-1997

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REFERENCE
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Best Local
Ouery Match
94.8%; Score 51; DB 6; Length 717;
Best Local Similarity 52.7%; Pred, No. 0.00017;
Matches 48; Conservative 18; Mismatches 25; Indels
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El (bases 1 to 717)

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El Hauer, W., Breckenridge, R., Cardinaux, F., Gombert, F., Gram, H.,

Ramage, P., Schneider, H., Waelchli, R., Albert, Rainer and Lewis, I.

ANALOGS OF PTH

Patent: WO 9402510-A 1 03-FEB-1994;

SANDOZ AG (AT)

Other publication HU 70459 951030

Other publication CZ 9500088 951018

Other publication NU 4156693 940120

Other publication NU 4156693 940120

Other publication NZ 248137 951221

Other publication NZ 248137 951221

Other publication NF 2269176 940202

Other publication NF 2269176 940202

Other publication NG 2100423 940116

Other publication CN 1099801 950308

Other publication DE 4393381T 950313

Other publication DE 4933381T 950313

Other publication NZ 9305126 950116

Other publication NZ 9305126 950116

Other publication NZ 9305126 950116
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Unclassified.
1 (bases 1 to 207)
1 (bases 1 to 207)
201denburg, K.R. and Selick, H.E.
Compounds with PTH activity
L. Patent: US 5814603-A 8 29-SEP-1998;
L. Contin e C
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101..562
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/codon start=1
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FNAFYQRGSIDPPSVSEIQLMENLGKHLNGMERVEWLRKKLQDVHNFVALG"
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Other publication HU 70459 951030
Other publication CZ 9500088 951018
Other publication SZ 9500088 951018
Other publication NZ 4156633 940120
Other publication NZ 4395 951027
Other publication NZ 269176 940202
Other publication CB 2269176 940202
Other publication CA 2100423 940116
Other publication CN 1099801 950308
Other publication EN 10930179 950427
Other publication DZ 950123 950315
Other publication NO 950123 950315
Other publication FJ 950121 950313.
Other publication FJ 950121 950313.
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   BD234383 405 bp DNA linear PAT 17-JUL-2003 Recombinant synthesis of beta-lipotropin and other peptides.
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Bauer, W., Breckenridge, R., Cardinaux, F., Gombert, F., Gram, H.,
Bauer, W., Schneider, H., Waelchli, R., Albert, Rainer and Lewis, I.
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Sequence 3 from Patent WO9402510.
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Patent: WO 9402510-A 3 03-FEB-1994;
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RTPGAEKKSYVDOSPSLDFLYEANDGSVNGPSVSEIQLMHNLGKHLNSMERVEMLRKK
LQDVHNFVALG"
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Recombinant synthesis of beta-lipotropin and other peptides
RECOMBINATE SYNTHESIS OF BETA-LIPOTROPIN AND CO
OS Artificial Sequence
PN JP 2002533072-A/4
PD 08-OCT-2002
PF 15-DEC-1999 US 60/113058
PR 21-DEC-1998 US 60/113058
PR 21-DEC-1998 US 60/113058
PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,
PI MICHAEL ANDREW MENKE
PC C12N15/09,C07K14/67,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
CC PC C12N15/10,C12N9/50,
PC C12N5/10,C12N9/50,
PC C12P21/02,C12N15/00,C12N5/00
CC Description of Artificial Sequence: PCpB-RVR-hPTH fusion FH
Key

CDS (4). (393).
                    other sequences; artificial sequences.

1 (bases 1 to 408)

Hale, J.E., Hershberger, C.L., Larson, J.L. and Recombinant synthesis of beta-lipotropin and Patent: JP 2002533072-A 6 08-OCT-2002; ELI LILLY AND CO

OS Artificial Sequence
PN JP 2002533072-A/6
PD 08-OCT-2002
PF 15-DEC-1999 JP 2000589671
PR 21-DEC-1998 US 60/113058
PI JOHN EDWARD HALE, CHARLES LEE HERSHBERG PI JOHN EDWARD HALE, CHARLES LEE HERSHBERG PI MICHAEL ANDREW MENKE
PC C12N15/09, C07K14/67, C07K19/00, C12N1/15, C12N15/00, C1
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synthetic construct
other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BD234383
BD234383.1 GI:33044153
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JP 2002533072-A/6.
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408 bp DNA
Recombinant synthesis of beta-lipotropin
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Similarity 52.2%; Pred. No. 0.00025;
48; Conservative 18; Mismatches 26;
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                                                                                                                                                                                          15-DEC-1999 JP 2000589671
21-DEC-1998 US 60/113058
JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,
MICHAEL ANDREW MENKE
C12N15/09, C07K14/67, C07K19/00, C12N1/15, C12N1/19, C12N1/21 PC
                              C12P21/02.C12N15/00.C12N5/00
Description of Artificial Sequence: PCpB-IEGR-hPTH fusion
Location/Qualifiers
CDS (4) (396)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Location/Qualifiers
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REFERENCE
AUTHORS
TITLE
JOURNAL
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BD234386
LOCUS
                                   RESULT 15
BD234384
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ORGANISM
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Best Local
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Matches 48; Conserv
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                                                                                        356 TAGAATGGCTGCGTAAGAAGCTGCAGGATGTT
                                                                                                                                    296 CTGTTTCTGAAATCCAGCTGATGCATAACCTGGGCAAACATCTGAACTCTATGGAGCGTG 355
                                                                                                     62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU : |||:|||:|||:|| ||:||:||| |:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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Recombinant synthesis of beta-lipotropin and other peptides. BD234384 BD234384.1 GI:33044154
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/mol_type="genomic DNA"
/db_xref="taxon;32630"
                                                                                                                                                                                                                                   /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                               54.2%; Score 50.4; DB 6; 52.2%; Pred. No. 0.00025; ive 18; Mismatches 26;
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Pred. No. 0.00025;
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SOURCE Synthetic construct

ORCANISM Synthetic construct

I (bases 1 to 411)

AUTHORS

FILL LILLY AND CO

OS Arctificial sequence

PN UP 2002533072-A 5 08-OCT-2002;

ELI LILLY AND CO

OS Arctificial sequence

PN UP 2002533072-A 5 08-OCT-2002;

PP 15-DEC-1990 UP 2000589671

PR 21-DEC-1990 UP 2000589671

PR
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	c 21	20	19	18	c 17	16	c 15	14	13	12	11	10	9	8	7	6	<sub>U</sub>	4	ω	2	۳	Result No.
36.6	37.2	38.2	38.2	38.2	38.2	38.2	38.2		38.2					38.2		38.2	38.2		38.8	38.8	40	Score
39.4	40.0	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.7	41.7	43.0	Query Match
523	780	820	809	757	741	721	702	583	576	536	496	453	450	434	416	411	376	352	324	316	339	Query Match Length
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W52945 zc03h08.rl	AI028087 ow51a12.x	BX103059 BX103059	BG188276 RST7292 A	BX106232 BX106232	AI051997 oy29c05.x	BG198564 RST17829	BH958789 odj08c01.	W39202 zb35h03.rl		W19765 zb39c03.rl	W56820 zc01a03 r1	W33077 zc07a12.rl	W56235 zc01e11.r1	W38764 zb27a07.rl	W31998 zb96d06.rl	W37708 zc10d12.rl	W38966 zb28b12 r1	W39062 zb34c06.r1	W19763 zb39c01.r1	AA372113 EST83976	T29548 EST83988 Hu	Description

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# ALIGNMENTS

	JOURNAL PUBMED COMMENT	TITLE	REFERENCE	RESULT 1 T29548 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)	Nature 377, 3-174 (1995) 7566098 Other_EST8: THC23168	Pellegrino, S.M., Phillips, Č.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, EJ., Dimke, D., Feng, P., Ferrite, A., Fischer, C., Hastings, G.A., He, WW., Hu, JS., Greene, J.M., Fischer, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, YF., Wing, J., Xu, C., Yu, GL., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Yu, GL., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Initial Assessment of Human Gene Diversity and Expression Patterns Based Tron 81 Million Hassesian of CDMA Sequence	Hominidae; Homo.  1 (bases 1 to 339)  Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,  Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,  Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,  White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, MW.,  Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,  FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,  Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkledr, P.S.,  Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,  Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,	729548 729548 739 bp mRNA linear EST 06-SEP-1995 EST83988 Human Parathyroid gland Homo sapiens cDNA 5' end similar to parathyroid hormone (HT:2194), mRNA sequence. 729548 729548.1 GI:611646 EST. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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RESULT 2
AA372113
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DEFINITION
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PUBMED
COMMENT
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source
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CE 1 (bases 1 to 316)

RAdams, M. D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Adams, M.D., Kerlavage, A.R., Sleischmann, R.D., Fuldner, R.A., Balt, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., White, O., Sutton, G., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Flizgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glock, A., Gnehm, C.L., Hanna, M.C., Hedblow, E., Hinkle, P.S., Jr., Kelley, J.C., Liu, L.-I., Marmarcas, S.M., Merrick, J.M., Schell, J.L., Saddek, D.M., Shirley, R., Shall, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Liv, Small, K.V., Spriggs, T.A., Utterback, T.R., Waidman, J.F., Liv, Small, K.V., Spriggs, T.A., Utterback, T.R., Waidman, J.F., Liv, Small, K.V., Spriggs, T.A., Utterback, T.R., Waidman, J.F., Liv, N., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.H., J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Fraser, C.M. and Venter, J.C.

Fraser, C.M. and Venter, J.C.

Fraser, C.M. and Venter, J.C.

Fraser, C.M. and Venter, J.C.

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Fraser, C.M. and Venter, J.C.

Fraser, C.M. and Venter, J.C.

Fraser, C.M. and Venter, J.C.

Fraser, J. A. J. A. L. A. Starter, J. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA372113 316 bp mRNA linear EST 21-APR-1997 EST83976 Parathyroid gland tumor II Homo saptens cDNA 5' end similar to parathyroid hormone, mRNA sequence.

AA372113 AA372113
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                                                 Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Location/Qualifiers
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//db_xref="AFCC (inhost):106648"
//db_xref="taxon:9606"
//clone_lib="Human_Parathyroid_gland"
/note="Organ: parathyroid_gland"
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Matches 44
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62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
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324 bp mRNA linear EST 03-MAY-1996
zb39c01.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE:305952 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
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1 (bases 1 to 324)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Huttman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Aikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Location/Qualifiers
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                                                                                                                                                                                                   /organism="Homo sapiens"
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/mol_type="mRNA"
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/db_xref="caxon:9606"
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/clone_lib="Soares_parathyroid_gland; Vector: pT7T3D
/note="Organ: parathyroid_gland; Vector: pT7T3D
/note="Organ: pT7T3D
/no
/organism="Homo sapiens".

mol type="mRNA"
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/dev stage="adult"
/clone_lib="Parathyroid gland tumor II"
/note="Organ: parathyroid gland; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
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48.4%; Pred. No. 0.29;
tive 14; Mismatches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further is
Seq primer: mob.REGA+ET
High quality seconsors
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352 bp mRNA linear EST 15-MAY-1990 zb34c06.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305482 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
Contact: Wilson RK
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TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3
                                                                 /lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares parathyroid tumor NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1:
Site_2: Eco RI; 1st strand cDNA was primed with
                                                                                                                                                                                                     /tissue_type="parathyroid tumor"
/dev stage="adult"
/lab_host="DH10B (ammirillin von
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/db_xref="GDB:1248892"
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/clone="IMAGE:305482"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zb28b12.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:304895 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                                                      TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento
                                                                                                                                                                                                                                          /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="GDB:1248305"
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                                                                                                                                                                                                                                                                                                           clone="IMAGE:304895"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. I
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1 (bases 1 to 411)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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411 bp mRNA linear EST 10-OCT-1996
zc11dd12.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE: 31911 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Fax: 314 286 1810
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/clone="IMAGE:321911"
/tissue type="parathyroid tumor"
/tissue type="parathyroid tumor"
/dey stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone lib="Soares parathyroid tumor MbHPA"
/clone lib="Soares parathyroid gland; VecTor: pT7T3D
/note="Torgan: parathyroid gland; VecTor: pT7T3D
(Pharmacia) with a modified polylinker; Site_1:
Site_2: Eco_RI; lst strand cDNA was primed with
                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1259569"
/db_xref="taxon:9606"
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Pred. No. 0.45;
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Soares and M.Fatima Bonaldo. RNA from sporadic parathyro adenomas was kindly provided by Dr. Stephen Marx, Nation Institute of Diabetes and Digestive and Kidney Diseases, NTH." parathyroid rx, National

Ş Query Match Best Local S Matches 44 N Similarity Conservative 41.18; Score 38.2; DI Pred. No. 0.45 14; Mismatches 38.2; No. 0. DB .45; 33; 8 Length Indels 0; Gaps 61 0;

210 62 uugaauggcugcguaaaaaacugcaggacgu CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 92

269

270 TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 300

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RESULT W31998 LOCUS DEFINITION W31998 Thear EST 20-AUG-199 mRNA linear EST 20-AUG-199 zb96d06.rl Soares parathyroid tumor NBHPA Homo sapieng cDNA clone IMAGE:320651 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence. EST 20-AUG-1996

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM W31998 W31998.1 EST. GI:1313010

Homo sapiens (human)

Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae; Homo. (bases 1 to 416)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlling, T., Schellenberg, K., Soares, M.B., Tan, F., Thlerry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

Contact: Wilson RK

Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

> <u>3</u> 63108

quality sequence stop: 386. Location/Qualifiers

source

/organism="Homo sapiens"
/mol type="mRNA"
/db xref="GDB:1258309"
/db xref="taxon:9606"
/clone="IMAGE:320651"

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/dev stage="adult"
/lab host="PH10B (ampicillin resistant)"
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/clone\_lib="Soares\_parathyroid\_tumor\_Site\_1"
/note="Organ: parathyroid gland; Vector: pT7T3D
/(Pharmacia) with a modified polylinker; Site\_1:
Site\_2: Eco RI; 1st strand cDNA was primed with Not I;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               w38764 434 bp mRNA linear EST 15-MAY-1990
zb27a07.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE:304788 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 434)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W38764.1 GI:1320471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 253.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                 TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3
                                                                                                       /tissue type="parathyroid tumor"
/dev_stage="adult"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares parathyroid tumor NbHPA"
/clone Tib="Soares parathyroid gland; Vector: pT7T3D
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site 1:
Site 2: Eco RI; 1st strand cDNA was primed with
                                                                                                                                                                                                                                                                                                               mol_type="mRNA"
/db_xref="GDB:1248198"
                                                                                                                                                                                                                                                                  clone="IMAGE:304788"
                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa;
                                                                                                                                                                                                                                                                                         xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.2; DB Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marra, M.,
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                                                                                                              Not I;
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RESULT
W56235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (inft@image.llnl.gov) for further information.
Insert Length: 865 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zc01e11.rl Soares parathyroid IMAGE:321068 5' similar to gb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W56235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W56235.1 GI:1358124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3
                                                                                                                     /tissue_type="parathyroid tumor"
/dev stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/clone="Organ: parathyroid gland; Vector: pT7T3D
/pharmacia) with a moddified polylinker; Site 1: Not 1;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                                                                         db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                     clone="IMAGE:321068"
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48.4%;
                                                                                                                                                                                                                                                                                                                                                            type="mRNA"
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Pred.
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vector (Pharmacia). Library went through one

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ACCESSION
VERSION
KEYWORDS
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AUTHORS
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W33077
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Best Local .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2007al1.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE.321598 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR W33077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 453)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Holman,M., Hiltman,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Seq primer: mob.REGA+ET
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                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 367
Location/Qualifiers
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314 286 1810
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                                                                                                                   /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:321598"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH1DB (ampicillin resistant)"
/lab_host="BH1DB (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid_gland; Vector: pT773D
(pharmacia) with a modified_polylinker; Site 1: Not
Site_2: Bco RI; 1st strand_cDNA_was primed_with a location_dmax.
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1. .453
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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//organism="Homo sapiens"
//organism="Homo sapiens"
//db_xref="GDB:1258662"
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Location/Qualifiers
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TTTTT-3'], double-stranded cDNA was size selected, lito Eco RI adapters (Pharmacia), digested with Not I ac cloned into the Not I and Eco RI sites of a modified vector (Pharmacia). Library went through one round of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W19765.1 GI:1295882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGÁTGGAGAGAG
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314 286 1810
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cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento
                                                                                                /clone="IMAGE:305956"
/tissue_type="parathyroid tumor"
/tissue_type="parathyroid tumor"
/dev stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid tumor_NbHPA"
/clone_lib="Soares_parathyroid_gland; Vector: pT7T3D
/note="Organ: parathyroid_gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco_RI; lst strand_cDNA was primed_with a Not I -
                                                                     to Eco RI adapters (Pharmacia),
                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249366"
/db_xref="taxon:9606"
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                                                                       double-stranded cDNA was size selected, ligatedapters (Pharmacia), digested with Not I and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 576)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hiller,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M
Holman,M., Hultman,M., Kucaba,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W56120.1 GI:1358009
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information Insert Length; 904 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 łomo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 433.
Location/Qualifiers
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                                                                                     /clone lib="Soares parathyroid tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site 1:
Site_2: Eco RI; 1st strand cDNA was primed with
                                                                  TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and
                                             cloned
                      vector (Pharmacia).
                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="GDB:1260565"
                                                                                                                                                                                                                                          /clōne="IMAGE:326363"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin_resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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into the Not I and Eco RI sites of a modified pT7T3 (Pharmacia). Library went through one round of ization to a Cot = 5. Library constructed by Bento
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a Not I -
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                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 583)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsonskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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583 bp mRNA linear EST 15-MAY-1996
zb35h03.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone
zMAGE:305621 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
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Location/Qualifiers
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Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
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Pred. No. 0.47;
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Best Local S
Matches 44
                                                                                                                                                            Query Match
Best Local Similarity
Matches 37; Conserv
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                                       GACATTGATÁCAAGA 592
                                                                     UGGCUGCGUAAAAAA 81
                                                                                                   TCTGCAGGCCATGAGATGCACGGTGGTGGTGGTGGTGGTTACTTCCCACGTGATGAG
                                                                                                                     UCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAA
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ACCESSION VERSION KEYWORDS

RESULT W39202 LOCUS

14

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Matches

DEFINITION

REFERENCE AUTHORS

COMMENT

FEATURES

Conservative

41.1%; Score 38.2; [ 49.3%; Pred. No. 0.49 tive 15; Mismatches

DB ,.49;

9;

Length Indels

23;

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Gaps

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adenomas was kindly provided by Dr. Institute of Diabetes and Digestive NIH." Stephen Marx, National and Kidney Diseases,

8

Length 583;

sequence. BH958789 Brassica oleracea
Brassica oleracea
Brassica oleracea
Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 702)
Delehaunty, K., Pewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K. High quality sequence start: 17
High quality sequence stop: 551.
Location/Qualifiers Plate: odj08 row: c column Seg primer: -21UPpOT forward Class: shotgun Contact: Richard K. Wilson Genome Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu Whole genome shotgun reads from Brassica oleracea Unpublished (2002) SSD BH958789.1 BH958789 702 bp DNA linear odj08c01.bl B.oleracea002 Brassica oleracea genomic, Similarity UUGAAUGGCUGCGUAAAAAACUGCAGGACGU TAGAATGGCTGCGTAAGAAGCTGCAGGATGT 143 CTGTGAGTGAAATACAGCTTATGCATAACCTGGGAAAACATCTGAACTCGATGGAGAGAG CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUGCAUGGAACGUG Conservative /organisme"Brassica oleracea"
/mol\_type="genomic DNA"
/db\_xref="taxon:3712"
/db\_xref="taxon:3712"
/clone lib="B.oleracea002"
/clone lib="B.oleracea002"
/note="Vector: poTwl3; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center." GI:23440016 41.1%; Score 48.4%; Pred. Mismatches 38.2; DB No. 0.48; 2 92 33; GSS 01-OCT-2002 0; Gaps 112 61 0

Search completed: November 24, 2005, 01:30:29 Job time : 1824 secs

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nucleic -

Sequence: Perfect score: Title:

Sequence Sequence

10, Appl 21, Appl 26, Appl 28, Appl 29, Appl 5, Appl 5, Appl

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Minimum DB seq
Maximum DB seq
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                                                                        No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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1: /cgn2 6/ptodata/1/ina/1 COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5—COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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US-08-468-275-5
US-09-007-466-3
US-09-007-466-5
US-09-007-466-5
US-08-952-980B-5
US-08-142-551B-8
US-08-133-446-58
US-08-689-190-1
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US-08-689-190-1
US-08-689-190-3
US-08-689-190-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Jung, Eun-Kyung
APPLICANT: Jung, Soo I1

APPLICANT: Park, Doo-Hong
APPLICANT: Chung, Soo I1

TITLE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE
TITLE REFERENCE: 0136/06626
CURRENT APPLICATION NUMBER: US/09/463,282D
CURRENT FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: PCT/KR98/00146
PRIOR APPLICATION NUMBER: PCT/KR98/00146
PRIOR APPLICATION NUMBER: WR 1997-35230
PRIOR FILING DATE: 1997-07-27
NUMBER OF SEQ ID NOS: 26
              Sequence 3, Application US/08468275
Patent No. 5747453
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 26
LENGTH: 258
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/09463282D Patent No. 6500647
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                       61.1%;
1 Similarity 54.3%;
50; Conservation
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US-08-835-231-6
US-09-108-661-6
US-09-108-661-6
US-09-949-016-18519
US-09-949-016-11793
US-09-949-016-11793
US-09-949-016-13712
                                                                                                                                                                                                                                                                                                                                                                                          20;
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Pred. No. 3.3e-09;
20; Mismatches 22
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Sequence 31, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 18519, A
Sequence 18519, A
Sequence 18719, A
Sequence 1170, Appl
Sequence 11712, A
Sequence 21, Appl
Sequence 21, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 28, Appl
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Result No.

score

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CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION

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RESULT 3
US-08-468-275-5/c
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AMME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEPAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/468,275
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
CLASSIFICATION: 514
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08468275
Patent No. 5747453
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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MOLECULE TYPE:
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 7.
ZIF: 94303-0802

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

ORBATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                            APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                              STREET: 950 PAGE MILL ROAD CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
LECULE TYPE: DNA (genomic)
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ZIP: 94303-0802
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CITY: PALO ALTO
                                                                                                                 COUNTRY:
                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 56.(
51; Conservative
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7..138
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25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360-0002;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
TELEPHONE: (415) 496-8150
TELEPHONE: (415) 496-8151
SEQUENCE CHARACTERISTICS:
LEMGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-468-275-5
US-08-468-275-5
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US-09-007-466-3
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                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/468,275
APPLICATION UNMER: US 08/468,275
PILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REGISTRATION NUMBER: 0360-0002;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: HOLLAD
APPLICANT: OLDENB
TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIF: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 58.3%; Score 54.2; DB 2;
Local Similarity 56.0%; Pred. No. 1.9e-08;
les 51; Conservative 17; Mismatches 23;
                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG
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OLDENBURG, KEVIN R.

VENTION: WETHOD FOR INCREASING THE

VENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                        US/09/007,466
                                                                                                                  O360-0002; ARC-2349
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Best Local :
Query Match
Best Local Similarity 56.0
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
                                                                                                                                     TELEFAX: (415) 496-8048 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/46E

PRILING DATE: 06-UN-1995

ATTORNEY, AGENT INFORMATION:

NAME: MILLER, D. BYRON

REGISTRATION NUMBER: 30,661

REFERENCE/DOCKET NUMBER: 0360

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 496-8150
                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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LOCATION:
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                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94303-0802
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                   TOPOLOGY: 11
                                                                                                           TYPE: nucleic acid
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                                                                                                                      ENGTH:
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CALIFORNIA
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                                                                                                                      141 base pairs
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25
                                                                                   linear
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                                                                    DNA (genomic)
                                                                                             single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHOD FOR INCREASING THE ELECTROTRANSPORT FLUX OF POLYPEPTIDES
 58.3%; Score 54.2; DB 3;
56.0%; Pred. No. 1.9e-08;
tive 17; Mismatches 23
                                                                                                                                                                                                                                                                             US 08/468,275
                                                                                                                                                                                                          O360-0002; ARC-2349
                            DB 3; Length 141;
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NAME: MILLER, D. BYRON

REGISTRATION NUMBER: 30,661

REFERENCE/DOCKET NUMBER: 2349

TELECOMMUNICATION INFORMATION:

TELEPAX: (650) 496-8048

INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08952980B Patent No. 6333189
                                                                                                                                     Query Match 58.3%; Score 54.2; DB 3; Best Local Similarity 56.0%; Pred. No. 1.9e-08; Matches 51; Conservative 17; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,980B
FILING DATE: 20-NOV-1997
CLASSIFICATION: 530
CLASSIFICATION: 530
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
                                                                                                                                                                                                                                                                   LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                         FEATURE:
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                26 CCGTTTCCGAAATCCAGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85
86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
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                                                                                                 2 CUGUTUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUGCAUGGAACGUG 61
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                                                                                                                                                                              Length 141;
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                                                                                                                                           Gaps
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RESULT 7 US-08-952-980B-5/c

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5, Application US/08952980B

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US-08-142-551B-8
; Sequence 8, Application
; Patent No. 5814603
; GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/952,980B
FILING DATE: 20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SBOUBANCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 496-8048 INFORMATION FOR SEQ ID NO: 5:
                                                                                              NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION INFORMATION
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ch 58.3%; Score 54.2; DB 3; Length 141; 1 Similarity 56.0%; Pred. No. 1. 19e-08; 51; Conservative 17; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94303-0802
                                                                                                                                                                                                                                                                                                                                                   Application US/08142551B
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ON: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/952,980B
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US-08-733-446-58
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Sequence 58, Application US/08733446
PATENT NO. 5856138
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS
TITLE OF INVENTION: PRODUCTION THEREOF
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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LENGTH: 207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-OCT-1992
ATTOREY/AGENT INFORMATION:
NAME: Swiss, Gerald F
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 0003
TBLECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 70...174
OTHER INFORMATION: /note= "Encodes the protein or
OTHER INFORMATION: peptide of interest"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 175..207
OTHER INFORMATION: /note= "Encodes amino acid sequence
OTHER INFORMATION: having six histamines that serves as a tag for the
OTHER INFORMATION: purification of the protein on a nickel column."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/142,551B FILING DATE: 25-0CT-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: 1..51
OTHER INFORMATION: /note OTHER INFORMATION: seque OTHER INFORMATION: inclu
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NAME/KEY:
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                                                                                                                                                                                                                                                  131 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 161
                                                                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                                                                        62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92
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ICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               58.3%; Score 54.2; DB 2; 56.0%; Pred. No. 2.2e-08; tive 17; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Encodes the leader peptide
sequence that serves to direct the
inclusion bodies."
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US-10-340-484-14
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                                                                                                                                                                                            Sequence 14, Applicate Patent No. 6875739
GENERAL INFORMATION:
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                                                                                                                    APPLICANT: Stewart, Andrew F.
TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501
                                                 CURRENT APPLICATION NUMBER: US/10/340,484
CURRENT FILLING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/347,215
PRIOR FILING DATE: 2002-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 1
FILING DATE:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 18-OCT-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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IDENTIFICATION METHOD:
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                APPLICATION NUMBER: 60/353,296 FILING DATE: 2002-02-01
APPLICATION NUMBER: 60/368,955
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                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
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nucleic acid
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SEQ ID NO 14
LENGTH: 102
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Patent No. 5714349
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                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/006,197
FILING DATE:
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PRIOR APPLICATION NUMBER: 60/379,125
PRIOR FILING DATE: 2002-05-08
                                                                               TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN TITLE OF INVENTION: PARATHYROID HORMONE NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    APPLICATION NUMBER: US/08/016,171
FILING DATE:
APPLICATION NUMBER: US/07/765,371
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D
REGISTRATION NUMBER: 30,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617)523-3400
 MOLECULE TYPE:
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                   TOPOLOGY:
                                 STRANDEDNESS:
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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                                                                 ENGTH:
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other nucleic acid, synthesizing DNA
                                   double
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49.5%; Pred. No. 2.5e-05;
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RESULT 12
US-08-733-446-23
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                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/733,446
FILING DATE: 18-CCT-1996
CLASSIFICATION: 43-5
PRIOR APPLICATION DATA: 45-5
PRIOR APPLICATION DATA: 45-5
PRIOR APPLICATION UMBER: US/08/402,970
FILING DATE: US/07/926,787
FILING
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GENERAL INFORMATION:
APPLICANT: FIDE
TITLE OF
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Best Local Similarity 49.5%;
Matches 45; Conservative 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA REJEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRATURE:

NAME/KEY: MUTATION

LOCATION: 7, 8, 9, 12, 15, 19, 21, 33, 36, 43, 51, 58, IDENTIFICATION METHOD: S
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        OLECULE TYPE:
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CITY: Boston
STATE: Massac
IDENTIFICATION METHOD:
                                                                                                         NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                TOPOLOGY:
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pred. No. 3.2e-05;
7; Mismatches 29;
                                                                                                                                                                                                                  synthetic
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Query Match 48.0%; Score 44.6; DB 2; Best Local Similarity 49.5%; Pred. No. 3.2e-05; Matches 45; Conservative 17; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEFAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucle
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
NAME/KEY:
LOCATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/402,970
FILING DATE:
APPLICATION NUMBER: US/07/926,787
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                           NAME/KEY: mutation
LOCATION: 103...105
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 18-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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5856138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRODUCTION THEREOF
62
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                                                                              Length 252;
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Gaps

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US-08-835-231-34
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                                                                                                                                                                                                                                      TELEFAX: 617-52.
TELEFAX: 200291 STRE
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 34
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
TYPE: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34,
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
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APPLICANT: NISHIM
                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: UFILING DATE: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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APPLICANT: FUKUDA, TSunehiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
                                                                                                      FEATURE:
                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                         MOLECULE TYPE: S
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                    NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/3 FILING DATE: 07-DEC-1994
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                                                                                                                        ORGANISM:
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                                                                                                                                                                                                                            TOPOLOGY: linear
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KURIYAMA, Masato
                                                                  Coding Sequence
                                                                                                                        Synthetic DNA
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                                                                                                                                                                                                          Synthetic DNA
   48.0%;
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                                                                                                                                                                                                                                                                                                                    34:
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 Score 44.6; DB 2;
Pred. No. 3.2e-05;
                   Length 252;
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US-09-108-661-34
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                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/838,857
APPLICATION NUMBER: JP 024841
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-CCT-1991
ATTORNEY/ACENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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             FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FUKUDA, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                      MOLECULE TYPE: S
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                                                                                                          NTI - SENSE:
                                                                                                                                                  STRANDEDNESS: dou
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 130 V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                            ORGANISM:
                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TAGAATGGCTGCGTAAGAAGTTGCAGGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTGTCCGAGATTCAGTTAATGCATAACCTTGGCAAACATTTGAACTCCATGGAGCGTG
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                                                                                                                                                                                                                                                                  617-523-6440
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KURIYAMA, Masato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                          ö
                                                           Synthetic DNA
                                                                                                                                                                                                                                                                                    617-523-3400
                Coding Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                        Synthetic DNA
                                                                                                                                                                       double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHOD FOR PRODUCING A BIOLOGICALLY ACTIVE RECOMBINANT CYSTEINE-FREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/108,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/350,709
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                                                                                                                                                                                                                                                                                                                   41614-FWC
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Run
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic -
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maximum
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  nucleic search, using
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Match
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93
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  GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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             US-10-997-078-60
US-10-997-700-33
US-10-997-700-34
US-10-997-700-141
US-10-997-700-35
US-10-997-700-35
US-10-997-700-89
US-10-997-700-75
US-10-997-700-75
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US-10-997-700-71
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US-10-997-700-93
US-10-997-70-98-14
US-10-407-078-43
US-10-407-078-43
US-10-407-078-43
US-10-848-279-8
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Sequence 60, Appl Sequence 31, Appl Sequence 61, Appl Sequence 62, Appl Sequence 62, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 13, Appl Sequence 75, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 78, Appl Sequence 79, Appl Sequence 79, Appl Sequence 70, Appl Sequence 14, Appl Sequence 18, Appli Sequence 19, Appli
                                                                                                                                                                                                                                                                                                       Description
 RESULT 2
US-10-997-700-33
; Sequence 33, Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
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US-10-997-078-60
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Publication No. US20050221444A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
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38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	39	39	40.8	43	44.2	44.2	44.6	47.6	47.6	47.6	47.6	47.6
41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.9	41.9	43.9	46.2	47.5	47.5	48.0	51.2	51.2	51.2	51.2	51.2
102	102	102	102	102	102	102	102	102	102	51	51	252	258	107	106	102	874	874	432	432	348
9	φ	9	9	9	9	9	9	9	9	w	w	7	8	W	ω	0	σ	0	σ	σ	σ
US-10-775-204-72	US-10-775-204-69	US-10-775-204-64	US-10-775-204-61	US-10-775-204-60	US-10-775-204-57	US-10-775-204-52	US-10-775-204-51	US-10-775-204-25	US-10-775-204-24	US-09-879-257A-52	US-09-879-257A-51	US-10-398-449-2	US-10-343-189-15	US-09-746-945-12	US-09-746-945-11	US-10-340-484-14	US-10-359-091-7	US-10-437-038-7	US-10-359-091-3	US-10-437-038-3	US-10-359-091-1
Sequence 72, F	Sequence 69, F	•	•	•	•	•	•	•	•	•	•	Sequence 2, A		•	•	Sequence 14, P	Sequence 7, Ap	Sequence 7, Ap	Sequence 3, Ap	Sequence 3, Ap	Sequence 1, Ap
Appl	Appi	Appl	Idda	Tddy	Appl	Tddy	Appl	Appl	Appl	rddy	Appl	Appii	Appi	Appl	Appl	Appl	tīđć	tīđċ	tIdo	Appli	Appli

ALIGNMENTS

#### ; FEATURE: ; OTHER INFORMATION: US-10-997-078-60 SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 60 LENGTH: 102 TYPE: DNA ORGANISM: Unknown Query Match Best Local Matches APPLICANT: Wagner, F. APPLICANT: Peng, L. APPLICANT: Xia, U. APPLICANT: Xia, U. APPLICANT: Holmquist, B. APPLICANT: Holmquist, B. APPLICANT: Restoragen, Inc. APPLICANT: Restoragen, Inc. CURRENT: REFERENCE: 1627.010US1 FILE REFERENCE: 1627.010US1 CURRENT APPLICATION NUMBER: US/10/997,078 CURRENT FILING DATE: 2004-11-24 PRIOR APPLICATION NUMBER: PCT/US03/16643 PRIOR APPLICATION NUMBER: PCT/US03/16643 PRIOR APPLICATION NUMBER: US/10/997,078 RIOR APPLICATION NUMBER: US/10/997,078 RIOR APPLICATION NUMBER: US/10/997,078 RIOR APPLICATION DATE: 2003-05-23 PRIOR APPLICATION DATE: 2003-05-24 NUMBER OF SEQ ID NOS: 148 62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93 ::|||:|||:|||:|||:|||:|||:||||||:: 62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93 l Similarity 53; Conservat CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG Conservative PTH(1-34). 64.5%; Score 60; DB 9; Le: 57.6%; Pred. No. 6.5e-11; or Mismatches 20; Length 102; Indels ٥, Gaps 61

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APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Holnquiet, B.
APPLICANT: Holnquiet, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypept:
PILE REFERENCE: 1627.009US1 US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR FILING DATE: 2004-11-24
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
FENORUM: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wagner, F
APPLICANT: Peng, L.
APPLICANT: Xia, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 61, Application US/10997078
Publication No. US20050221444A1
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Best Local Similarity
                                                                                                                                                           Matches
                                                                                                                                                                                             Query Match
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APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Wethods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627.010US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,370
RIOR APPLICATION NUMBER: US 60/383,370
RIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 61 LENGTH: 111
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 102
TYPE: DNA
ORGANISM: Unknown
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  62
               62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93 ::|||:|||:|||:||||::
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                                                                                                                                                                             Similarity
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                                                                                                                                                           Conservative
                                                                                                                                                    64.5%; Score 60; DB 9; Length 111; 57.6%; Pred. No. 6.6e-11; tive 19; Mismatches 20; Indels
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CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGUCCAUGGAACGUG

19;

Indels

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Gaps

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APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
FILE REFERENCE: 1627.09US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTMARE: FasteBQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 111
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US-10-997-700-34
                                                                                 ; FEATURE:
; OTHER INFORMATION: A synthetic PTH sequence.
US-10-997-078-141
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; OTHER INFORMATION: PTH(1-37)
US-10-997-700-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 141, Application US/10997078
publication No. US20050221444A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
    Query Match
Best Local Similarity
Matches 53; Conserv
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Best Local
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TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic FILE REFERENCE: 1627.010US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION UNUMBER: PCT/US03/16643
PRIOR FILING DATE: 2003-05-23
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                TYPE: DNA
ORGANISM: Artificial
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53; Conserva
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No. US20050239172A1
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          64.5%; ilarity 57.6%; Conservative 1
                                                                                                                                     Sequence
        Score 60; DB 9
Pred. No. 6.7e-
19; Mismatches
DB 9; b. 6.7e-11;
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ches 20;
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                                          Length 117;
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SEQ ID NO 35
LENGTH: 252
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: F
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US-10-997-078-62
Sequence 62, App
Publication No.
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APPLICANT: Yia, U.
APPLICANT: Yia, U.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627,010US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR SEQ ID NOS: 148
NUMBER OF SEQ ID NOS: 148
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Weng, L.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
APPLICANTION: Methods and DNA Constructs for High Yield Production of Polypepti
FILE REFERENCE: 1627-009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
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                           PTH(1-84)
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57.6%;
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Pred. No. 8e-11;
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GENERAL INFORMATION:
APPLICANT: Seo, Jin Seog
APPLICANT: Strydom, Daniel
APPLICANT: Holmquist, Barton
APPLICANT: Holmquist, Barton
APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Polypeptide Cleavage Process
FILE REFERENCE: 1627.026US1
CURRENT APPLICATION NUMBER: US/10/997,762
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16468
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US-10-997-700-89
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US-10-997-762-18
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PRIOR PRILING DATE: 2004-11-24
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.
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APPLICANT: Peng, L
APPLICANT: Xia, U.
APPLICANT: Holmqui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 89, Application US/10997700 Publication No. US20050239172A1
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 276
                                                                                                                                                                                                                                                                                                      Sequence 18, Ap
Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                    PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR FILING DATE: 2002-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods
FILE REFERENCE: 1627.009US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/997,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 264
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: A synthetic pBN121-M-PTH(1-84)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU ::|||:|||:||:::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGGAACGUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG 64
                                                                                                                                                                                                                                                                                                        Application US/10997762
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57.6%;
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57.6%;
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Pred. No. 8e-11;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60; DB 9;
Pred. No. 8.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Sequence 3, Application US/10997822
Publication No. US20050227314A1

GENERAL INFORMATION:
APPLICANT: Holmquist, B.
APPLICANT: Strydom, D.
APPLICANT: Genealk, X.
APPLICANT: Cryer, R.
TITLE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS
FILE REFERENCE: 1627.011US1
CURRENT APPLICATION UNMBER: US/10/997,822
CURRENT FILING DATE: 2004-01-24
PRIOR APPLICATION NUMBER: PCT/US03/16647
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,484
PRIOR FILING DATE: 2003-05-24
NUMBER OF SEQ ID NOS: 9
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 276
TYPE: DNA
ORGANISM: Artificial Sequence
Sequence 75, Application US/10997700
Publication No. US20050239172A1
GENERAL INFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Yia, U.
APPLICANT: Holmquist, B.
ITILE OF INVENTION: Methods and DNA Constructs for FILE REFERENCE: 1627.009US1
FILE REFERENCE: 1627.009US1
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US/60/383,212
PRIOR FILING DATE: 2002-05-24
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US-10-997-822-3
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                  173
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                                                                                                                                                                                                                                                                                                           233 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                             62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 57.6
53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUGCCAUGGAACGUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.5%; Score 60; DB 9; 57.6%; Pred. No. 8.2e-11;
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57.6%; Pred. No. 8.
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8.2e-11;
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                                                                                             High Yield Production of Polypept:
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US-10-997-700-76
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        APPLICANT: Wagner,
APPLICANT: Peng, L
APPLICANT: Xia, U.
APPLICANT: Holmqui
                                                                            Sequence 76, Application US/10997700 Publication No. US20050239172A1 GENERAL INFORMATION:
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; FEATURE:
; OTHER INFORMATION: A
US-10-997-700-75
                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: A
US-10-997-078-133
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                                                                                                                                        Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                   APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
APPLICANT: Restoragen, Inc.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic FILE REFERENCE: 1627.010US1
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR PRILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 133
SEQ ID NO 133
SEQ ID NO 133
SEQ ID NO 133
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Best Local S
Matches 53
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SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 75
LENGTH: 276
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 133, Application US/10997078
Publication No. US20050221444A1
GENERAL IMFORMATION:
APPLICANT: Wagner, F.
APPLICANT: Weng, L.
APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial
                                                                   227 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 258
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                                                                                                                                                             Similarity
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::|||:|||:|||:|||||||||::
TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 105
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57.6%;
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                                                                                                                                          64.5%; Score 60; DB 9; L
57.6%; Pred. No. 8.2e-11;
tive 19; Mismatches 20;
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Pred. No. 8.2e-11
9; Mismatches 2
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                                                                                                                                              Indels
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                                                                           226
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Peng, L. Xia, U. Holmquist,

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FILE REFERENCE: 1677.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for FILE REFERENCE: 1677.009US1
CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: US 60/383,212
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
SEQ ID NO 77
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US-10-997-700-77
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                                                                        US-10-997-700-91
                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                      US-10-997-700-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 77, Application US/10997700 Publication No. US20050239172A1 GENERAL INFORMATION:
                  Sequence 91, Application US/10997700 Publication No. US20050239172A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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APPLICANT: Wagner, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: A synthetic PCR product.
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89
                                                                                                                                                                                                                               29
                                                                                                                                                                                       62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                   2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGUUCCAUGGAACGUG
                                                                                                                                                                                                                                                                                                         53; Conservative
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|||:|||:|||:|||:|||||:||||::
TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 120
                                                                                                                                                  TTGAATGGCTGCGTAAAAACTGCAGGACGTT 120
                                                                                                                                                                                                                               CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                       64.5%; Score 60; DB 9;
57.6%; Pred. No. 8.3e-11;
tive 19; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                              DB 9; Length 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for High Yield Production of Polypept
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                 88
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FEATURE:
, OTHER INFORMATION: A synthetic pBN121-T7tag-CH-PTH(1-84). US-10-997-700-91
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APPLICANT: Xia, U.
APPLICANT: Xia, U.
APPLICANT: Holmquist, B.
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic
TITLE OF INVENTIAL METHOD
TO SEPECT ON METHOD

SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMENT OF SEPTIMEN
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Best Local Similarity
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TYPE: DNA
ORGANISM: Artificial Sequence
122
                                                                                               62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                               62 CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 9; we pred. No. 8.5e-11; wismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9; Length 321;
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Search completed: November 24, 2005, 04:46:56 Job time: 413.667 secs

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OM nucleic -
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic search, using sw model
Published_Applications_NA_New:*

1: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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Gapop 10.0 , Gapext 1.0
         1987.5.22
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93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3205263 seqs, 74304013 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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22 23	18 19 20	15 16	12	10	4006	3 2 P	ult No.
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US-10-839-799-28 US-10-858-730-35 US-10-689-742-77	-10-821-234-2 -10-502-893-1 -10-972-766-1	-10-509-921-1 -10-509-921-1	100	US-10-509-422-1 US-10-509-422-3 US-11-005-030-1 US-10-667-295-44	US-10-485-517-4 US-10-927-641-116 US-10-821-234-318 US-10-821-234-255	US-10-821-234-760 US-10-821-234-839 US-10-392-234A-15	Ιΰ
Sequence 28, Appl Sequence 35, Appl Sequence 77, Appl	e 226	11,	1, 11	Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 44, Appl	Sequence 4, Appli Sequence 116, App Sequence 318, App Sequence 255, App	Sequence 760, App Sequence 839, App Sequence 15, Appl	Description

23.7 2043 1 23.7 2745 9 23.7 2748 9 23.7 2850 9 23.7 2850 9 23.7 2850 9 23.4 3160 8 23.4 5796 1 23.4 5796 1 23.0 2458 1 23.0 2458 1 23.0 3305 7 23.0 3305 7 23.0 12391 7 23.0 12391 7 23.0 12391 7 23.0 12391 7 23.0 12391 7 23.0 3308 1 23.8 1392 1 23.8 1392 1 23.8 1392 1 23.8 1392 1	22 23.7 2043 1 US-10-46/-ysc26-150 22 23.7 2631 9 US-11-077-550-65 22 23.7 2727 9 US-11-077-550-63 22 23.7 2748 9 US-11-077-550-67 22 23.7 2748 1 US-10-821-234-662 22 23.7 2850 9 US-11-077-550-67 22 23.7 3939 9 US-11-077-550-67 22 23.7 3393 9 US-11-112-944-8 21.8 23.4 3160 8 US-11-112-944-8 21.8 23.4 5796 1 US-10-821-234-62 21.6 23.2 809 8 US-11-131-826A-387 21.4 23.0 2458 1 US-10-131-826A-387 21.4 23.0 2458 1 US-10-131-826A-387 21.4 23.0 3305 7 US-10-0821-234-267 21.4 23.0 3371 1 US-10-131-826A-35 21.4 23.0 3371 7 US-11-017-550-67 21.4 23.0 12391 7 US-11-040-159-127 21.2 22.8 3328 1 US-10-793-626-349 21.2 22.8 3370 1 US-10-793-626-3392 21.2 22.8 4035 1 US-10-793-626-3392	Ω		ი		ი				O					Ω							a	Ω
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7 2634 9 1 7 2727 9 9 7 2727 9 9 7 2745 9 9 7 2745 9 9 7 2745 9 9 7 2745 9 9 7 2745 9 9 7 2745 9 9 7 2745 9 9 7 2745 9 9 7 2745 9 9 7 2745 9 1 2 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	7 2631 9 US-11-077-550-65 Sequence 7 2631 9 US-11-077-550-65 Sequence 7 2727 9 US-11-077-550-65 Sequence 7 2748 9 US-11-077-550-63 Sequence 7 2748 9 US-11-077-550-67 Sequence 7 2748 1 US-10-821-234-662 Sequence 7 2850 9 US-11-077-550-67 Sequence 7 3393 9 US-11-077-550-67 Sequence 8 196 1 US-10-821-234-62 Sequence 9 2743 1 US-10-131-826A-251 Sequence 17 2748 1 US-10-131-826A-267 Sequence 17 2748 1 US-10-131-826A-367 Sequence 17 2743 1 US-10-131-826A-35 17 27 US-11-017-550-67 Sequence 17 2743 1 US-10-793-626-349 Sequence 17 2743 1 US-10-793-626-349 Sequence 17 2743 1 US-10-793-626-3525 Sequence 17 2750 1 US-10-793-626-3525 Sequence 17 2750 1 US-10-793-626-3525 Sequence 18 3701 1 US-10-793-626-3525 Sequence	21.2	21.2	21.2	21.2	21.2	21.4	21.4	21.4	21.4	21.4	21.4	21.6	21.6	21.8	21.8	22	22	22	22	22	22	22
	9 US-11-077-550-65 9 US-11-077-550-65 9 US-11-077-550-63 9 US-11-077-550-63 9 US-11-077-550-67 9 US-11-077-550-67 9 US-11-077-550-67 9 US-11-077-550-138 9 US-11-077-550-138 9 US-11-112-944-8 9 US-11-112-826A-251 1 US-10-131-826A-387 1 US-10-131-826A-35 1 US-10-131-826A-35 1 US-10-131-850-67 1 US-11-017-550-67 1 US-11-017-550-67 1 US-11-017-550-67 1 US-11-017-550-67 1 US-11-017-550-67 1 US-11-040-1159-127 1 US-11-040-1159-127 1 US-10-793-626-349 1 US-10-793-626-3525 1 US-10-793-626-3525 9 Sequence 9 US-10-793-626-3525 9 Sequence 9 US-10-793-626-3525 9 Sequence 9 US-10-793-626-3525	22.8	22.8	22.8	22.8	22.8	23.0	23.0	23.0	23.0	23.0	23.0	23.2	23.2	23.4	23.4	23.7	23.7	23.7	23.7	23.7	23.7	23.7
9 US-11-077-550-65 9 US-11-077-550-65 9 US-11-077-550-63 9 US-11-077-550-67 9 US-11-077-550-67 9 US-11-077-550-138 8 US-11-112-944-8 1 US-10-821-234-62 1 US-10-821-234-66 1 US-10-131-826A-25 1 US-10-131-826A-267 1 US-10-131-826A-387 1 US-10-131-826A-35 1 US-10-93-626-349 1 US-10-793-626-3392 1 US-10-793-626-3392	1-077-550-65 1-077-550-65 1-077-550-65 Sequence 1-077-550-67 Sequence 0-821-234-662 Sequence 1-1077-550-67 Sequence 1-1077-550-67 Sequence 1-112-944-8 Sequence 1-12-94-8 Sequence 1-131-826A-251 Sequence 0-821-234-62 Sequence 0-821-234-67 Sequence 0-821-234-267 Sequence 0-131-826A-367 Sequence 0-131-826A-367 Sequence 0-131-826A-367 Sequence 0-821-234-267 Sequence 0-131-826A-35 Sequence 0-133-626-349 Sequence 0-793-626-3392 Sequence 0-793-626-3392 Sequence	4035	3701	3328	1392	59	12732	12391	3371	3305	2743	2458	1714	809	5796	3160	3393	2850	2748	2745	2727	2631	2043
US-11-07-550-65 US-11-077-550-65 US-11-077-550-63 US-11-077-550-67 US-11-077-550-67 US-11-077-550-67 US-11-077-550-67 US-11-12-944-8 US-11-132-839-6 US-11-131-826A-387 US-10-131-826A-387 US-10-131-826A-387 US-10-131-826A-387 US-10-131-826A-387 US-10-131-826A-387 US-10-131-826A-387 US-10-131-826A-387 US-10-131-826A-387 US-10-131-826A-35 US-11-017-550-67 US-11-040-159-127 US-11-040-159-139-626-3392 US-10-793-626-3392	1-077-550-65 1-077-550-65 1-077-550-65 Sequence 1-077-550-67 Sequence 0-821-234-662 Sequence 1-1077-550-67 Sequence 1-1077-550-67 Sequence 1-112-944-8 Sequence 1-12-94-8 Sequence 1-131-826A-251 Sequence 0-821-234-62 Sequence 0-821-234-67 Sequence 0-821-234-267 Sequence 0-131-826A-367 Sequence 0-131-826A-367 Sequence 0-131-826A-367 Sequence 0-821-234-267 Sequence 0-131-826A-35 Sequence 0-133-626-349 Sequence 0-793-626-3392 Sequence 0-793-626-3392 Sequence	1	_	<u> </u>	1	7	μ,	7	μ	7	μ	_	<u>, .</u>	œ	_	8	9	ø	_	9	9	9	۳
		US-10-793-626-3525	US-10-793-626-3392	US-10-793-626-3644	US-10-793-626-349	US-11-040-159-127	US-10-802-796-1	US-11-017-550-67	US-10-131-826A-35	US-11-017-550-68	US-10-821-234-267	US-10-131-826A-387	US-10-131-826A-251	US-11-132-839-6	US-10-821-234-62	US-11-112-944-8	US-11-077-550-138	US-11-077-550-67	US-10-821-234-662	US-11-077-550-59	-		US-10-46/-962B-100

#### ALIGNMENTS

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US-10-821-234-839
; Sequence 839, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-760
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US-10-821-234-760/c
                                                                                                                                                                                                                                RESULT 2
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Publication No. US20050255114A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: pt_SEQ_genes Version 1.0 SEQ ID NO 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
NUMBER OF SEQ ID NOS: 1704
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macun 30.5%; Score 28.4; DB 1; Length 2327; Local Similarity 44.9%; Pred. No. 0.82; es 35; Conservative 12: Migmathin.
                                                                                                                                                                                                                                                                                                       834 GAGGATCTGCTGCAGGTT 817
                                                                                                                                                                                                                                                                                                                                                                                                          894 CAGCTGCCCCCTGGGTGGTGGAGGCCGTGACGACCATGATGGTGGCATTGGT 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 CAGCUGAUGCACGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGU 75
                                                                                                                                                                                                                                                                                                                                                      76 AAAAAACUGCAGGACGUU 93
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT EILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 839
SEQ ID NO 839
SEQ ID NO 839
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US-10-485-517-4
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US-10-392-234A-15/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Homo sapiens US-10-821-234-839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-392-234A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pharmacia and Upjohn Corporation
APPLICANT: Buxser, Steven
APPLICANT: Buxser, Steven
APPLICANT: Docle, Keith
APPLICANT: Docker, Douglas
APPLICANT: Atazini Li
TITLE OF INVENTION: Method for Screening for acrab Transporter Family Inhibitors
FILE REFERENCE: 6206
CURRENT APPLICATION NUMBER: US/10/392,234A
CURRENT FILING DATE: 2003-03-17
PRIOR FILING DATE: 2002-03-15
RIUNG FOR SEQ ID NUMBER: US 60/364,935
PRIOR FILING DATE: 2002-03-15
SUMMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 3138
                                                          Sequence 4, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/10392234A
Publication No. US20050255538A1
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Best Local
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Best Local S
APPLICANT: Foster, Simon APPLICANT: Mond, James TITLE OF INVENTION: Antique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 26.5%;
Local Similarity 41.3%;
les 26; Conservative 13
OF INVENTION: Antigenic Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3204 ATG 3206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 TGCACGGCGATGGCCGGCGGGGCGATGGCCGGGTACTGGTTGACCGGCAGACTGAGGATC 78
                                                                                                                                                                                                                                                                                    83 UGCAGGACG 91
                                                                                                                                                                                                                                                                                                                                                                      23 UGCACGGUGGUGGUGGUGGUGGUUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAAC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 UUÇ 64
                                                                                                                                                                                                                                               77 GACAGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                           ch 26.0%; Score 24.2; I Similarity 50.7%; Pred. No. 21: 35; Conservative 6; Mismatches
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Pred. No. 18;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 6497;
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FITTLE OF INVENTION: MODILICATION CONTROL FILE REFERENCE: 11000.103664
CCURRENT APPLICATION NUMBER: US/10/927,641
CCURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US. NO. 09/724,624
PRIOR APPLICATION NUMBER: U.S. NO. 09/598,401
PRIOR APPLICATION NUMBER: U.S. NO. 60/146,591
PRIOR APPLICATION NUMBER: U.S. NO. 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: U.S. NO. 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 143
SOPTWARE: PastSEQ for Windows Version 4.0
FEGITH: 947
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: P100629WO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 5690
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Sequence 116, Application US/10927641
Publication No. US20050244968A1
GENERAL INFORMATION:
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                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-927-641-116

// TYPE: DNA
// ORGANISM: Staphylococcus aureus
US-10-485-517-4

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Best Local S
Matches 27
                                                                                     Matches
                                                                                                      Query Match
Best Local
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APPLICANT: Eagleton, Clare
APPLICANT: Lasham, Annette
APPLICANT: Wood, Marion
APPLICANT: Wood, Marion
APPLICANT: Wisser, Elizabeth
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 25.6%; Score 23.8; Local Similarity 40.3%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520 GETGTTTCCGGCTCGCTTGGTACTTCTGGTGTCGCTGGCGTTGGTGGCACGATTGGAGGT 579
528 ATGGTGGTGGTGGTGGTGGTGGTGGTGAA 488
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                                      27;
                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                     25.2%;
llarity 51.2%;
Conservative
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                                                                                Score 23.4; DI
Pred. No. 29;
9; Mismatches
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                                                                                                                            DB 1;
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                                                                                     11;
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                                                                                                                            Length 947;
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RESULT 8
US-10-509-422-1/c
US-10-509-422-1/c
; Sequence 1, Application US/10509422
; Publication No. US20050244825A1
; Publication No. US20050244825A1
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; ORGANISM: Homo sapiens
US-10-821-234-318
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-255
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human BMP2 Inducible Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _ENGTH: 1657
                                                                                                                                                                                                                                                                                     / Match 24.9%; Score 23.2; DB 1; Length 3893;
Local Similarity 43.2%; Pred. No. 47;
nes 19; Conservative 12; Mismatches 13; Indels 0
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                                                                                                                                                                                                  2665 TTCCGGAGGTGATGATGGTGGTGGTGGTGGTGGTGGT 2622
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                                                                                                                                                                                                                         5 UUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGUGGU 48
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o. US20050255114A1
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o. US20050255114A1
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; Pred. No. 33;
5; Mismatches
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RESULT 10 US-11-005-030-1/c

GENERAL INFORMATION

APPLICANT: Aerssens, Jeroen APPLICANT: Athanasiou, Mar APPLICANT: Brain, Carlos

Maria

APPLICANT:
APPLICANT:

APPLICANT:

Denton, R. Rex Judson, Richard S. Cohen, Nadine Dain, Bradley Brain, Carlos

Reed, Carol R.

Sequence 1, Application US/11005030 Publication No. US20050255495A1

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FILE REFERENCE: 004974.01015
CURRENT APPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: PCT/EP03/080825
PRIOR APPLICATION NUMBER: US 60/367,512
PRIOR FILING DATE: 2003-03-27
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/406,936
PRIOR APPLICATION NUMBER: US 60/406,936
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; ORGANISM: Homo sapiens US-10-509-422-1
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    문
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US-10-509-422-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10509422
Publication No. US20050244825A1
GENERAL INFORMATION:
APPLICANT: Liou, Simon
TITLE OF INVENTION: Human BMP2 Inducible Kinases
                                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 3704
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                         Query Match 24.7%; Score 23; DB Best Local Similarity 46.8%; Pred. No. 54; Matches 22; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/EP03/080825
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/367,512
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/406,936
PRIOR FILING DATE: 2002-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 004974.01015
CURRENT APPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2004-09-24
                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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|:| : | | | | | |:
1609 CIGCIGCATATAAGCATCTTGAAGTAGGTGGTGGTGGTGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGU 48
                                              2 CUGUUUCCGAAAUCCAGCUGAUGCACGGUGGUGGUGGUGGUGGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.7%; Score 23; DB 1; Length 3507; 46.8%; Pred. No. 53;
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Sequence 44, Application US/10667295

Publication No. US20050257293A1

GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
ITILE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERRENCE: 11696-047001

CURRENT PILICATION NUMBER: US/10/667,295

CURRENT FILING DATE: 2003-09-17

PRIOR APPLICATION NUMBER: US 60/411,823

PRIOR APPLICATION NUMBER: US 60/411,823

PRIOR FILING DATE: 2002-09-17

NUMBER OF SED ID NOS: 26

SOFTWARE: FASCSEQ for Windows Version 4.0

SEQ ID NO 44

LENGTH: 481

TYPE: DNA
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CURRENT APPLICATION NUMBER: US/11/005,030

CURRENT FILING DATE: 2004-12-07

PRIOR APPLICATION UNUMBER: US 60/529,999

PRIOR FILING DATE: 2003-12-15

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.3

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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LOCATION: (16546)..(16546)
OTHER INFORMATION: n is 'g' or 'a'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 26323
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc feature
LOCATION: (1973)..(1973)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (16520)..(16520)
OTHER INFORMATION: n is 'c'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOCATION: (2273)..(2273)
OTHER INFORMATION: n is 'a'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (2010)..(2010)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (2010)..(201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (2273)..(227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 24.7%;
Socal Similarity 47.9%;
ss 34; Conservative
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Pred. No. 83;
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  Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/021,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 119
SEQ ID NO 119
LENGTH: 2218
FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
US-10-509-921-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-10-821-234-119/c
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, NAME/KEY: misc feature

; LOCATION: (1)...(481)

; OTHER INFORMATION: Ceres Seq. ID no. 6425497

US-10-667-295-44
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                                                                                                                                                                                                                                                                            Sequence 9, Application US/10509921
publication No. US20050250093A1
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicans
FILE REFERENCE: P51335
CURRENT APPLICATION NUMBER: US/10/509,921
CURRENT FILING DATE: 2004-10-01
CURRENT FILING DATE: 2004-10-01
                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/369,685
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 119, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Labat, APPLICANT: Stack
                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                          LENGTH: 7979
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Local Similarity 51.4%;
Local Similarity 51.4%;
les 19; Conservative
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                       The polynucle otide sequence encodes sequences from HCV {\it J4}\,({\it B/RI}) Replicons
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24.3%;

Score 22.6; Pred. No. 86;

DB 1;

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Sequence 11, Application US/10509921

Publication No. US20050250093A1

GENERAL INFORMATION:

APPLICANT: SmithKline Beecham Corporation

TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons

FILE REFERENCE: P51335

FURRENT APPLICATION NUMBER: US/10/509,921

CURRENT FILING DATE: 2004-10-01

PRIOR APPLICATION NUMBER: 60/369,685

PRIOR APPLICATION NUMBER: 60/369,685

PRIOR APPLICATION NUMBER: 60/369,685

PRIOR APPLICATION NUMBER: 0/369,685

PRIOR A
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US-10-509-921-11/c
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                                                                                                                                                   PEATURE:
OTHER INFORMATION: Thepolynucleotide sequence encodes sequences
OTHER INFORMATION: HCV J4 Replicons
US-10-509-921-11
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Publication No. US20050250093A1
GENERAL INFORMATION:
APPLICANT: SmithRline Beecham Corporation
TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
FILE REFERENCE: P51335
FILE REFERENCE: P51335
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Best Local Similarity 43.5%; Pred. No. 86;
Matches 30; Conservative 10; Mismatches
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LENGTH: 7979
Query Match 24.3%; Score 22.6; DB 1; Best Local Similarity 43.5%; Pred. No. 86; Matches 30; Conservative 10; Mismatches 29;
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PRIOR APPLICATION NUMBER: 60/369,685
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
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   29;
                                                                             Length 7979;
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Title:
Perfect score:
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: gb ba:*
2: gb in:*
3: gb om:*
4: gb om:*
5: gb po:*
5: gb pt:*
6: gb pt:*
7: gb pt:*
7: gb sts:*
7: g
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
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o S	48.4	52.0	74	0	AR043802	
σ	46.2		141	6	AR005132	
c 7	46.2	9	141	σ	AR005133	AR005133 Seque
ω	46.2	49.7	141	σ	AR177779	AR177779 Seque
0			141	σ	AR177780	AR177780 Seque
10	46.2	49.7	207	σ	AR043797	AR043797 Seque
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12	44.6		945	6	A36849	A36849 Sequenc
13	44	47.3	405	თ	BD234383	BD234383 Recon
14	44	47.3	408	0	BD234385	BD234385 Recom
15	44	47.3	408	σ	BD234386	BD234386 Recon
16	44	47.3	411	σ	BD234384	BD234384 Recon
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42.8			42.8			42.8	42.8	42.8	42.8	42.8	42.8	42.8	42.8	42.8	42.8	42.8	42.8	42.8	42.8	44.5	46.2	46.2	46.7	46.7	47.3	47.3
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E05667	AR027016	E05666	AR027015	E05665	AR027014	E05660	AR027013	E05659	AR027012	E05664	AR027010	E05663	AR027009	E05662	AR027008	E05676	E05661	AR027049	AR027007	BD234410	AR135774	A79761	AR269023	BD073301	BD234389	BD234388
E05667 DNA encodin	AR027016 Sequence	E05666 DNA encogin	AR027015 Sequence	E05665 DNA encodin	AR027014 Sequence	E05660 DNA encodin	AR027013 Sequence	E05659 DNA encodin	AR027012 Sequence	E05664 DNA encodin	AR027010 Sequence	E05663 DNA encodin	AR027009 Sequence	E05662 DNA encodin	AR027008 Sequence	E05676 DNA encodin		AR027049 Sequence	AR027007 Sequence	BD234410 Recombina	AR135774 Sequence		()			

# ALIGNMENTS

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Query Match	ORIGIN	Source								COMMENT	COMMENT	JOURNAL		TITLE	AUTHORS	Collegeded	ORGANISM	SOURCE	KEYWORDS	VERSION		LOCUS	BD266834	RESULT 1
th 100.0%; Score 93; DB 6; Length 93;	/mor_ype- yenomic nam /db_xref="taxon:32630"	LOCALIDI/QUAITILEES  1. 93  /organism="synthetic construct"  /mol type="genomic DNA"	FT source 193	C12N1/21, C12N1/21, C12N1/21,	A61P19/10, PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC	JUEPPNER PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P5/18,A61P19/08, PC	MAS J GARDELLA,	PF 30-DEC-1999 JP 20005911/1 PR 31-DEC-1998 US 60/114577	08-OCT-2002		THE GENERAL HOSTITAL CORF	Patent: JP 2002533115-A 3 08-OCT-2002;	ligand-receptor molecules	Q.	Gardella, T.J., Kronenberg, H.M., Potts, J.T. and Jueppner, H.	Other sequences; artificial sequences.	synthetic construct	synthetic construct	JP 2002533115-A/3.	BD266834.1 GI:33076602	thered ligand-receptor molecules.	BD266834 93 bp kNA linear FAI 1/-001-2003		

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   BD266833 93 bp RNA linear PAT 17-JUL-2003 PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules. BD266833 BD266833 GI:33076601 JP 2002533115-A/2.
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PC C12N1/21,
PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC PC C12N5/10,G1N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC Description of Artificial Sequence: modified PTH sequence FH Key Location/Qualifiers
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PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules
Patent: JP 2002533115-A 1 08-OCT-2002;

THE GENERAL HOSPITAL CORP
OS Artificial Sequence
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PF 30-DEC-1999 JP 2000591171
PR 31-DEC-1999 US 60/114577
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1 (bases 1 to 93)
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PTH functional domain conjugate peptides, derivatives thereof and
novel tethered ligand-receptor molecules.
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/mol_type="genomic RNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 258)
Jung,E.-K., Park,D.-H. and Chung,S.-I.
Recombinant expression vector of human parathyroid hormone
Patent: US 6500647-A 26 31-DEC-2002;
Mogam Biotechnology Research Institute; Kyonggi-Do;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR269042 258 bp
Sequence 26 from patent US 6500647.
AR269042
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larity 51.1%;
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/db_xref="taxon:32630"
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                                                                             ; Score 53.6; DB 6;
; Pred. No. 4.6e-05;
21; Mismatches 24;
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; Pred. No. 3.7e-08;
21; Mismatches 18;
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                                                                                                                               Length 258;
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Oldenburg,K.R. and Selick,H.E.
Compounds with PTH activity
Patent: US 5814603-A 132 29-SEP-1998;
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AR005133
Sequence 5 from
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TTGAATGGCTGCGTAAAAAACTGCAGGATGTT
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                                                              TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
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/mol_type="unassigned DNA"
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/mol_type="unassigned
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Pred. No. 0.0064;
l6; Mismatches 28;
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Pred. No. 0.0015;
2; Mismatches 1;
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Holladay,L.A. and Oldenburg,K.R.
Method for increasing the electrotransport
Patent: US 5747453-A 5 05-MAY-1998;
Location/Qualifiers
                                                                                                                                                                                                     2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUCGGAACUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 141)
Holladay, L.A. and Oldenburg, K.R.
Method for increasing the electrotransport
Patent: US 6313092-A 3 06-NOV-2001;
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/mol_type="unassigned DNA"
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Pred. No. 0.0064;
6; Mismatches 28;
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Pred. No. 0.0064;
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1 Similarity 51.6%;
47; Conservation
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unclassified sequences.

1 (bases 1 to 717)
Bauer, W., Breckenridge, R., Cardinaux, F., Gombert, F., Gram, H.,
Bauer, W., Breckenridge, R., Cardinaux, F., Albert, Rainer and Lewis, I.
Ramage, P., Schneider, H., Waelchli, R., Albert, Rainer and Lewis, I.
ANALOGS OF PTH
Patent: WO 9402510-A 1 03-FEB-1994;
SANDOZ AG (AT)
Other publication HU 70459 951030
Other publication CZ 9500088 951018
                                                                                                                                                                                                                                                                                                        717 bp
Sequence 1 from Patent WO9402510.
A36847
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Method for increasing the electrotransport flux of polypeptides
Patent: US 6313092-A 5 06-MOV-2001;
Location/Qualifiers
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/mol_type="unassigned DNA"
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; Pred. No. 0.0065;
16; Mismatches 28;
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                                                                                                        unclassified sequences.

1 (Dases 1 to 945)

Bauer, W., Breckenridge, R., Cardinaux, F., Gombert, F., Gram, H.,

Ramage, P., Schneider, H., Waelchli, R., Albert, Rainer and Lewis, I

ANALOGS OF PTH

L Patent: WO 9402510-A 3 03-FEB-1994;

SANDOZ AG (AT)

Other publication CZ 9500088 951018

Other publication AU 4156693 940120

Other publication AU 4156693 940120

Other publication NZ 248137 951221

Other publication NZ 248137 951221

Other publication NZ 248137 951221

Other publication NZ 248137 95000

Other publication CA 2100423 94010

Other publication CA 2100423 94010

Other publication CN 1099801 950308

Other publication DB 6194198 94070

Other publication NZ 430517 950313

Other publication NZ 9303126 950116

Other publication NZ 9303126 950116

Other publication PR 1950771 950313.

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Sequence 3 from Patent WO9402510.
A36849 GI:2294107
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FNAFVQRGSIDPPSVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALG"
     /organism="unidentified"
/mol_type="unassigned DNJ
/db_xref="taxon:32644"
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/mol type="unassigned DNA"
/db_xref="taxon:32644"
/01__562
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49.5%; Pred. No. 0.019;
tive 17; Mismatches 29;
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1 (bases 1 to 405)

2 (bases 1 to 405)

2 (bases 1 to 405)

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                             UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
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21-DEC-1998 US 60/113058
JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON, MICHAEL ANDREW MENKE
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FNAFVQRIKKERKEVAKKYSYTQSWKQEWIADGIEASITOLMHNICKHINGMERUEWLIRKK
FNAFVQRIKKERKEVAKKYSYTQSWCONYDSWCOTOLMHNICKHINGMERUEWLIRKK
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ENCE 1 (bases 1 to 408)

FORS Hale, J.E., Hershberger, C.L., Larson, J.L. and Menke, M.A.

Recombinant synthesis of beta-lipotropin and other peptides

ELI LILLY AND CO

SArtificial Sequence
PN JP 2002533972-A/7

PD 08-OCT-2002

PR 15-DEC-1999 JF 2000589671

FR 12-DEC-1999 JG 60/113058

PI JOHN EDWARD HALE, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON,
PI MICHAEL ANDREW MENKE
PC C12N15/09, CO7K14/67, CO7K19/00, C12N1/15, C12N1/12 PC

C12N5/10, C12N9/50,
PC C12P21/02, C12N15/00.C12NF/00
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JP 2002533072-A/7
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15-DEC-1999 JP 2000589671
21-DEC-1999 US 60/13058
JOHN EDWARD HALB, CHARLES LEE HERSHBERGER, JEFFREY LYNN LARSON, MICHAEL ANDREW MENKE
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21-DEC-1998 US 60/113058
JOHN EDWARD HALE,CHARLES LEE HERSHBERGER,JEFFREY LYNN LARSON,
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/mol_type="genomic DNA"
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Adg48059 Human mut
Adg68786 Human mut
Adg93179 Novel exp
Adj65857 PTH pepti
Adw14377 Human par
Adg93180 Novel exp
Adj65858 PTH pepti
Adw14375 Human par
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Adj65858 PTH prote
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Adj65813 Tandem po
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New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.

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                                                                                                             (GARD/)
(KRON/)
(POTT/)
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                                                                       Gardella TJ,
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) KRONENBERG H M.
) POTTS J T.
) JUEPPNER H.
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New compound comprising an amino terminal signaling functional domain

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Synthetic.
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     WPI; 2000-452384/39
P-PSDB; AAY96975.
                                                                                                                        (GARD/)
(KRON/)
(POTT/)
(JUEP/)
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) KRONENBERG H M.
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                                                                                                                                                                                                                                                                                                          99WO-US031108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "PG7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 73.8; DB 3;
Pred. No. 2.5e-13;
0; Mismatches 12;
                                                                               Potts JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 U; 0 Other;
                                                                               Jueppner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 93;
                                                                               Η;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reformation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding
R_1 is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 4
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new S is an amino terminal signaling functional domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT73910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT73910 standard; DNA; 152 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 93
                                                                                                                                               06-NOV-1996;
                                                                                                                                                                                                                                                                WO9718314-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
                              (BOEF )
                                                                                     16-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                              BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GUUGAAUGGCUGCGUAAAAAACUGCAGGACGUU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 1; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligonucleotide encoding linker and PTH 1-37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          production; endoproteinase LysC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 19 A; 16 C; 33 G; 0 T; 25 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                        95DE-01042702.
                                                                                                                                               96WO-EP004850.
                                                                                                                                                                                                                                                                                                                                                                     /note= "5' end of complementary strand overhangs 3' of present strand by sequence 5'-TCGA-3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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Pred. No. 2.5e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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CC The present sequence, which encodes a linker and the parathyroid hormone CC 1-37 (PTH 1-37) peptide with codon usage optimised for E. coli, was CC ligated to the 2.9 kb NheI-HindIII fragment of pSAM-CCRE, which contains CC the Met (13-139) streptavidin (SA) sequence, to give pSA-EK-PTH. pSA-EK-CC PTH and the LacIq repressor plasmid pUBS500 were used to transform E. CC coli K12 RM82. The transformants were grown, with IPTG induction, in CC medium containing kanamycin and amplicilin. Cells were harvested, lysed CC and isolated inclusion bodies solubilised in guanidine hydrochloride, and CC renatured by dilution in pH 7 phosphate buffer. The solution was CC clarified and the supernatant concentrated and purified on a column of CC mmobbilised iminobiotin. The purified material was incubated with CC fragment removal on an iminobiotin column followed by chromatography on a CC fractogel and reverse phase HPLC. The endoproteinase LysC cleaves the CC fusion protein rapidly and completely, exclusively at the Lys residue in CC the linker, i.e. not at Lys residues in SA. (Updated on 25-MAR-2003 to CC correct pR field)
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Best Local
                                                                                                                                                                                 thrombocytopaenia; megakaryocyte deficiency; platelet deficiency; thrombocytopaenia; aplastic anaemia; idiopathic thrombocytopaenia; metastatic tumours; systemic lupus erythematosus; splenomegaly; fanconi's syndrome; vitemin B12 deficiency; folic acid deficiency; May-Hegglin anomaly; Miskott-Aldrich syndrome; paroxysmal nocturnal haemoglobinuria; glucagon-like peptide 1; GLP-1; non-insulin dependent diabetes; haemostatic; dermatological; immunosuppressive; antiinflammatory; cytostatic; mutant; variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant production of peptide(s) as fusions with streptavidin attached via cleavable linker - especially for urotropin and parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW21946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 152 BP; 44 A; 38 C; 35 G; 35 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 2; 37pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hormone production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kopetzki E;
                                                                                                                                                                                                                                                                                                                                                                               Human PTH-TTR (C10A/K15A/G83C) variant fusion DNA
03-APR-2003; 2003US-00407078
                                     16-OCT-2003
                                                                                                                                                                   parathyroid
                                                                                                                                                                                                                                                                                                                                       Transthyretin; TTR; thrombopoietin mimetic peptide; TPO; TMP
                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG48030 standard; DNA; 489
                                                                         US2003195154-A1
                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linker, i.e. n
mect PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGTTTCCGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCCATGGAACGTG
                                                                                                                                                                     hormone; PTH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.3%;
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Pred. No. 1.8e-06;
7; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 152;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method of increasing the serum half-CC life of a biologically active agent involves fusing the biologically CC active agent to transthyretin (TTR) or a TTR variant. The method is useful for increasing the serum half-life of a biologically active agent. CC Homogenous compositions comprising thrombopoietin (TPO) mimetic peptide CC (TMP) is useful for treating thrombocytopaenia, megakaryocyte/platelet CC deficiency/thrombocytopaenia, dispathic thrombocytopaenia, megakaryocyte/platelet CC deficiency famound; syndrome, vitamin B12 deficiency, folic acid CC splenomegally, Fanconi's syndrome, vitamin B12 deficiency, folic acid CC splenomegally, Fanconi's syndrome, vitamin B12 deficiency, folic acid CC deficiency, May-Hegglin anomally, Wiskott-Aldrich syndrome and paroxysmal CC nocturnal haemoglobinuria. Homogenous compositions comprising glucagon-CC like paptide 1 (CLP-1) is useful for treating non-insulin dependent CC diabetes. TMP compounds are useful in stimulating certain cell types CC other than megakaryocyte, which expresses Mp1 receptor and in maintaining CC the viability or storage life of platelets and related cells. The present CC sequence is human parathyroid hormone (PTH)-TTR variant fusion DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                                                                                                                                                                                                                                      Transthyretin; TTR; thrombopoietin mimetic peptide; TPO; TMP; thrombocytopaenia; megakaryocyte deficiency; platelet deficiency; thrombocytopaenia; aplastic anaemia; idiopathic thrombocytopaenia; metastatic tumours; systemic lupus erythematosus; splenomegaly; metastatic tumours; systemic lupus erythematosus; splenomegaly; Fanconi's syndrome; vitamin B12 deficiency; folic acid deficiency; May-Hegglin anomaly; Wiskott-Aldrich syndrome; paroxysmal nocturnal haemoglobinuria; glucagon-like peptide 1; GLP-1; non-insulin dependent diabetes; haemostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Increasing serum half-life of biologically active agent involves fusing biologically active agent to transthyretin or a transthyretin variant.
                                                                                                                                                                                       immunosuppressive; antiinflammatory; cytostatic; mutant; variant; parathyroid hormone; PTH; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-2002; 2002US-00117109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PTH-TTR (C10A/K15A/A81C) variant fusion DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG48059 standard; DNA; 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WALK/) WALKER K. (XION/) XIONG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
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47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96
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51.1%;
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Pred. No.
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les 25;
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US2003195154-A1

US2003191056-A1 Homo sapiens. Human; transthyretin; TTR; gene; ss; TPO mimetic peptide; TMP; thrombocytopenia; aplastic anaemia; metastatic tumour; cancer;

cytostatic; mutant

antianaemic;

Human mutant transthyretin (TTR)

CDNA #12.

64 61

11-MAR-2004

(first entry)

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RESULT 7
ADG68786
ID ADG6
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ADG
XX
ADG
AX
ADG
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CC life of a biologically active agent involves fusing the biologically
CC active agent to transthyretin (TTR) or a TTR variant. The method is
CC useful for increasing the serum half-life of a biologically active agent
CC (Homogenous compositions comprising thrombocytopaenia, megakaryocyte/platelet
CC (TMP) is useful for treating thrombocytopaenia, megakaryocyte/platelet
CC (CTMP) is useful for treating thrombocytopaenia, megakaryocyte/platelet
CC (CTMP) is useful for treating thrombocytopaenia, megakaryocyte/platelet
CC (CTMP) is useful for treating thrombocytopaenia, metastatic tumours
CC (CTMP) in thrombocytopaenia, systemic lupus erythematosus,
CC splenomegaly, Fancon's syndrome, vitamin B12 deficiency, folic acid
CC deficiency, May-Hegglin anomaly, Wiskott-Aldrich syndrome and paroxysmal
CC deficiency, May-Hegglin anomaly, Wiskott-Aldrich syndrome and paroxysmal
CC curnal haemoglobinuria. Homogenous compositions comprising glucagon-
CC like peptide 1 (GLP-1) is useful for treating non-insulin dependent
CC diabetes. TMP compounds are useful in stimulating certain cell types
CC ther than megakaryocyte, which expresses Mp1 receptor and in maintaining
CC the viability or storage life of platelets and related cells. The present
CC sequence is human parathyroid hormone (PTH)-TTR variant fusion DNA.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG68786 standard; cDNA; 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
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47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGAATGGCTGCGTAAGAAACTGCAGGACGTT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xiong F;
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Pred. No. 2.3e
20; Mismatches
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2.3e-06;
25;
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RESULT 8
ADG93179
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AC ADG9
XX ADG9
XX ADG9
XX Nove
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XX VAN
DE Nove
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression cassette; high yield polypeptide production; tandem polypeptide; inclusion body; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating thrombocytopenia, comprises fusing the agent to transthyretin a variant of it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG93179 standard; DNA; 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 14; 35pp; English
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                                Harley S,
                                                                                                                                                                                        24-MAY-2002; 2002US-0383370P
                                                                                                                                                                                                                                                      23-MAY-2003; 2003WO-US016643
                                                                                               (REST-) RESTORAGEN INC. (HARL/) HARLEY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-010111/01
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                                    JA,
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51.1%; Pred. No. 2.3e-06;
tive 20; Mismatches 25
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                                    Xia
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RESULT 9
ADJ65857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 200
P-PSDB;
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P-PSDB; ADG93159.
The invention comprises an expression cassette which produces a tandem polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide
                                                                                                                                                                                                                                                                                          New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression cassette; tandem polypeptide; inclusion body; inclusion body fusion partner; PTH; gene; ds.
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                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xia Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2002; 2002US-0383212P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2003; 2003WO-US016645.
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les 48; Conserv
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DB; ADJ65837.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT
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                                                                                                                                                                                                 SEQ ID NO 33; 132pp; English.
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Pred. No. 5.1e-06
8; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 T; 0 U; 0 Other;
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Best Local :
                                                                                                                                                                                                                                                                                                            The invention relates to a novel process for preparing recombinant human parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADM14376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADM14378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the PTH 1-34 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a peptide which may be used in the construction of a tandem polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 102 BP; 30
                                                                                                                                                                                                                                                                     Sequence 102 BP; 30 A; 24 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3; 25pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Production of reorganized human parathyroid hormone 1-34 peptide
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DB; ADW14378.
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                            UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                     CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
                                                                                                                                    CUGUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUCGUCUGAACUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xiu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
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Pred. No. 5.1e-
18; Mismatches
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Pred. No. 5.1e-06;
8; Mismatches 26;
                                                                                                                                                                                                                                                                     22 G; 26 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                       Length
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102;
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RESULT 12
ADJ65858
ID ADJ6
XX
AC ADJ6
XX
DT 06-N
XX
DE PTH

ADJ65858;

ADJ65858

standard;

DNA;

111

ВР

PTH peptide 06-MAY-2004

coding sequence

#2

(first

entry)

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> 61 61

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RESULT 11
ADG931LT
ADG931LT
ADG93
ID 9 ADG93
XX ADG93
XX 11-N2
XX VOVel
XX VOVel
XX VOVel
XX Unide
XX Unide
XX Unide
XX Unide
XX Unide
XX VA CRES
PR 23-N2
XX VA CRES
PR WPI;
DR WPI;

                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette produces a tandem polypeptide that forms an inclusion body when expressed in a cell. The expression cassette is useful for producing peptide and polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The producing peptide and inclusion body when expressed in a cell. The present sequence is that of a DNA sequence which encodes a polypeptide which may be produced using the expression cassette of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New expression cassette comprising an operably linked nucleic acid sequence, useful for producing a tandem polypeptide that forms an inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel expression cassette-related polypeptide-encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 111 BP; 30 A; 26 C; 25 G; 30 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 61; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harley S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2002; 2002US-0383370P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003100021-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ADG93160
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(HARL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2003; 2003WO-US016643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004-035128/03
62
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HARLEY S.
                                                                                                                                                                                                                                                                                                  Similarity
                                  UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                           CUGUUUCCGAAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
                                                                                                                          TGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams
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                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                           54.2%; Score 50.4; DB 12; 52.2%; Pred. No. 5.2e-06; tive 18; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luan
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93
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RESULT 13
ADM14375
ID ADM14
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XX ADM14
XX IO-MA
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide that form an inclusion body when expressed in a cell. The expression cassette of the invention is useful for producing a peptide or polypeptide in a cell, preferably a tandem polypeptide that forms an inclusion body when expressed in a cell. The present DNA sequence encodes a peptide which may be used in the construction of a tandem polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 34; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence, useful for producing a tandem polypeptide that forms
inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New expression cassette comprising an operably linked nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-035129/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xia Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-2002; 2002US-0383212P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-2003; 2003WO-US016645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises an expression cassette which produces
                                                 12-DEC-2001; 2001CN-00142627.
                                                                                                   12-DEC-2001; 2001CN-00142627
                                                                                                                                                                                                    CN1424325-A.
                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                     ds; parathyroxin;
                                                                                                                                                                                                                                                                                                                                                     Human parathyroxin Gly-Ser-Pro-PTH 1-34 peptide DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                         10-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADW14375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADW14375 standard; DNA; 111
                                                                                                                                                     18-JUN-2003
     (SHAN-) SHANGHAI BIOLOGICAL ENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUGUTUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.2%;
ilarity 52.2%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 30
                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                     recombinant protein; protein engineering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50.4; DI
Pred. No. 5.2e
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
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     RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coduces a tandem in a cell. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parathyroxin 1-34 peptide, including such steps as culturing a host cell in proper conditions, separating Gly-Ser-Pro-PTH 1-34 peptide (ADW14376), severing by Pro endopeptidase to form PTH 1-34 peptide (ADW14378) and separating and purifying PTH 1-34 peptide. The present sequence encodes the Gly-Ser-Pro-PTH 1-34 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 111 BP; 31 A; 28 C; 25 G; 27 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 1; 25pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of reorganized human parathyroid hormone 1-34
                                                                    New expression cassette comprising an operably linked nucleic sequence, useful for producing a tandem polypeptide that forms inclusion body when expressed in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-2004
This invention relates to a novel expression cassette and methods for high yield production of polypeptides. The cassette comprises an operably linked nucleic acid sequence, where the expression of the cassette
                                                                                                                                                                                                                                                                                                                                                     expression cassette; high yield polypeptide production; tandem polypeptide; inclusion body; gene; ds; PTH.
                                                                                                                                                                                                                                                                                                                                                                                      Novel expression cassette-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG93260
                                                Disclosure;
                                                                                                                    WPI; 2004-035128/03.
P-PSDB; ADG93259.
                                                                                                                                                        Harley S, Williams
                                                                                                                                                                                                                    24-MAY-2002; 2002US-0383370P
                                                                                                                                                                                                                                          23-MAY-2003; 2003WO-US016643
                                                                                                                                                                                                                                                                  04-DEC-2003.
                                                                                                                                                                                                                                                                                          WO2003100021-A2
                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                 (HARL/)
                                                                                                                                                                                             (REST-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                   polypeptide;
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                                                                                                                                                                                 RESTORAGEN
HARLEY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADW14376
                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTTTCTGAAATCCAGCTGATGCACAACCTGGGTAAACACCTGAACTCTATGGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUGUUUCCGAAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ntx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 102
                                                SEQ ID NO 141; 157pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ú
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                          Luan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50.4; DB 13;
Pred. No. 5.2e-06;
8; Mismatches 26;
                                                                                                                                                          ָש
                                                English.
                                                                                                                                                                                                                                                                                                                                                                                        PTH DNA SeqID141.
                                                                                                                                                          Xia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
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Matches 48
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                                      A portion (AAT34865) of plasmid pBN1:PTH(1-34)C-1c comprises DNA coding for a fusion protein (AAR87867) composed of the C-terminal end of human carbonic anhydrase II joined by an intraconnecting peptide (including a thrombin cleavage site) to amino acids 1-34 of PTH (AAR88966), followed by a Cys residue and C-terminal sequence. The complete construct can be expressed in E. coli transformants. The intraconnecting peptide and C-terminal Cys residue enable the recombinant protein construct to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTH; parathyroid hormone; parathormone; C-amide; C-amidated peptide; alpha-carboxamide; recombinant protein; fusion protein; transpeptidation; vector; plasmid pBN1; carbonic anhydrase II; ss.
                                                                                                                                                                              Example 7; Fig 1; 93pp; English.
                                                                                                                                                                                                                                 Production of C-terminal alpha-carboxamidated peptide(s) - by cleavage and transpeptidation of recombinant multicopy peptide(s) or fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 BP; 35 A; 27 C; 25 G; 30 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:||:||:|||:|||||||::
62 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
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Similarity 52.2%;
48; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pBN1:PTH(1-34)C-1c portion encoding PTH(1-34)Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIGITICIGAAATCCAGCIGAIGCACAACCIGGGIAAACACCIGAACICTAIGGAACGIG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..162
/*tag= a
/product= "hCA-linker-PTH(1-34)Cys fusion"
                                                                                                                                                                                                                                                                                                                                        Heriksen DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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Pred. No. 5.3e-06;
8; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                        Holmquist B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                        Wagner FW;
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Matches 48
                                                                                                                             Sequence 168 BP; 41 A; 44 C; 42 G; 41 T; 0 U; 0 Other;
62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
::|||:|||:|||:||||||||||:1
107 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 138
                                          47
                                                                N
                                                                                               Similarity
                                         CUGUUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGAACCUCCAUGGAACGUG
                                                                                     Conservative
                                                                                              54.2%;
                                                                                   Score 50.4; DB 2;
Pred. No. 5.7e-06;
8; Mismatches 26;
  138
                                                                                                        Length 168;
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                                                                                     Gaps
                                             106
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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                       Searched:
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  EST: *

1: 9b

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7: 9b

7: 9
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    November 23, 2005, 22:36:53 ; Search time 1823 Seconds (without alignments) 2386.834 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                    41078325 seqs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                                                                           US-09-475-158A-16
93
                                                                                                                                                                                                                                                                                                                                                                                         1 gcuguuuccgaaaucggugg.....guaaaaaacugcaggacguu 93
gb_est1...*
gb_est2...*
gb_htc.....*
gb_est6...*
gb_est6...*
gb_est6...*
gb_est6...*
gb_gss2...*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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38.2	38.2	œ	œ	œ	38.2	8	38.2		•	38.2		•	38.2	•	38.2		œ	38.2	8	38.8	39.2	Score
41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1	41.1		41.1	41.1	41.1	41.1		41.1	41.1	41.1	41.1		42.2	34
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BG188276	AI028087	BX106232	AA843660	AI051997	BG198564	AA788985	W39202	W56120	W52795	W19765	W52945	W56820	W33077	W56235	W38764	W31998	W37708	W38966	W39062	W19763	AI909008	ID
BG188276 RST7292 A		BX106232 BX106232	AA843660 ak08g07.s	AI051997 oy29c05.x	BG198564 RST17829	AA788985 ah29c05.s	W39202 zb35h03.rl	W56120 zc56h06.rl	W52795 zc02b12.rl	W19765 zb39c03.rl	W52945 zc03h08.rl	W56820 zc0la03.rl	W33077 zc07a12.r1	W56235 zc0le11.r1	W38764 zb27a07.rl	W31998 zb96d06.rl	W37708 zc10d12.rl	÷	W39062 zb34c06.rl	W19763 zb39c01.rl	00	Description

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ω.	٠,	34	34	34.2	34.2	34.4	34.6	34.6	34.8	34.8	35	35	35.4	35.6	35.6	35.8	36.2	36.6	36.6	36.6	37.2	38.2
36.6	36.6	36.6	36.6	36.8	36.8	37.0	37.2	37.2	37.4	37.4	37.6	37.6	38.1	38.3	38.3	38.5	38.9	39.4	39.4	39.4	40.0	41.1
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BU008102	B0861241	BU005353	BQ987803	CK481107	BZ137695	BE360066	CW921961	CNS02QMI	CG442723	CR159040	AI031553	BE212803	CO984533	AA771739	CC894877	CA184654	T29548	AA843141	CF231132	AA772070	AA372113	BX103059
٠	BQ861241 QGC17020.	BU005353 QGG7N20.y	BQ987803 QGF13D16.				-		CG442723 OGTAUI/TV		AI031553 ow48c08.x		CO984533 GM8901382				T29548 EST83988 Hu	AA843141 ak06c02.s				

## ALIGNMENTS

נו מ	FEATURES SOUTCE	JOURNAL PUBMED COMMENT	REFERENCE AUTHORS TITLE	RESULT 1 A1909008 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
/organism="Homo sapiens" /mol_type="mRNA" /mol_type="mRNA" /db xref="taxon:9606" /db xref="taxon:9606" /sex="female" /dev_stage="Adult" /clone_lib="BT197" /note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2:	Hrazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br Email: asimpson@ludwig.org.br Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome This sequence was derived from the following URL (http://www.ludwig.org.br/seq/gethtml.pl?ti=QV&t2=QV-BT197-038.html &t3=050499&t4=1) \$eq primer: puc 18 forward. Location/Qualifiers 1527	sequence rays Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 10737800 Contact: Simpson A.J.G. Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,	l (bases 1 to 527)  1 (bases 1 to 527)  2 (bases 1 to 527)  3 (bases 1 to 527)  3 (bases 1 to 527)  3 (bases 1 to 527)  4 (bases 1 to 527)  3 (bases 1 to 527)  4 (bases 1 to 527)  5 (bases 1 to 527)  4 (bases 1 to 527)  5 (bases 1 to 527)  6 (bas	A1909008 A1909008 QV-BT197-050499-038 BT197 Homo sapiens cDNA, mRNA sequence. A1909008 A1909008.1 GI:6499688 EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hommo sapiens Eukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae. Homo.

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae, Homo.

(bases 1 to 324)

Hillier, L., Clark, N., Dubuque, T., Elliston, Holman, M., Hultman, M., Kucaba, T., Le, M., Lé
Parsons, J., Rikkin, L., Rohlfing, T., Soares, Trevaskis, E., Waterston, R., Willamson, A., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Finail: est@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 222.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W19763
324 bp mRNA linear EST 03-MAY-1996
zb39e01.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE: 5 similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W19763.1 GI:1295880
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/tisuse_type="parathyroid tumor"
//dev stage="adult"
//dev stage="adult"
//lab_hoste="DHJDB (ampicillin resistant)"
//lab_hoste="DHJDB (ampicillin resistant)"
//clone_lib="Soares_parathyroid_gland; Vector: pT7T3D
//note="Organ: parathyroid_gland; Vector gland; Vector 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249362"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="IMAGE:305952"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.2%;
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Pred. No. 0.32;
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Le,M., Lennon,G., Marra,M.,
Soares,M., Tan,F.,
Soares,M., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω,
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              Query Match
Best Local Similarity
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REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

FEATURES

41.18;

Score 38.2; DB Pred. No. 0.61;

8

RESULT W19763

N

LOCUS DEFINITION

5

Matches

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TITLE
JOURNAL
COMMENT
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
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W39062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
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Best Local S
Matches 33
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100 TCTGAACTCGATGGAGGAGGATGTTGCTGCGTAAGAANCTGCAGGATGT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project
Unpublished (1995)
Contact wilson RK
Contact wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.

1 (Dases 1 to 352)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Hillier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M.

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zb34c06.rl Soares parathyroid tumor NDHPA Homo sapiens cDNA clone IMAGE:305482 5' sīmilar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 41.7%;
l Similarity 64.7%;
33; Conservative 1
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W39062.1 GI:1320771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 286.
Location/Qualifiers
                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="myBil248892"
/db_xref="raxon:9606"
/clone="IMAGE:305482"
/tissue_type="parathyroid tumor"
/tissue_type="parathyroid tumor"
/dev stage="adult"
/lab_host="MHOBE (ampicillin resistant)"
/lab_host="MHOBE (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/clone_lib="Soares_parathyroid_gland; Vector: pT773D
/note="Organ: parathyroid gland; Vector: pT773D
/note="Organ: parathyroid fumor_NbHPA"
/note="Cogn: parathyroid gland; Vector: pT773D
(pharmacia) with a modified polylinker; Site 1: Not I;
Site_2: Boo RI; 1st strand cDNA was primed with a Not I -
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38.8; DB Pred. No. 0.4; 0; Mismatches
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RESULT W38966

SOURCE

Wohldmann, P. and

Marra, M.,

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밁 5

linear

EST 10-OCT-1996

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REFERENCE
AUTHORS
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VERSION
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DEFINITION
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1 (bases 1 to 376)

1 (bases 1 to 376)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               w38966 376 bp mRNA linear EST 15-MAY-199 zb28b12.r1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE.304895 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W38966.1 GI:1320674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: mob.REGA+ET
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                                                                                                                                  Similarity
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                     UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92

    est@watson.wustl.edu
clone is available royalty-free through LLNL; contact the
E Consortium (info@image.llnl.gov) for further information.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                          Conservative
                                                                                                                                                                                                                                        TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                Institute
NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid_gland; Vector: pT773D
/note="Organ: with a modified polyllnker; Site 1: Not I;
(Pharmacia) with a modified polyllnker; Site 1: Not I;
Site_2: Eco RI; lst strand cDNA was primed with a Not I -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1248305"
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                                                                                                                               41.1%;
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                                                                                                                             Score 38.2; DB Pred. No. 0.62;
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AUTHORS
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KEYWORDS
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W37708
RESULT
W31998
LOCUS
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Matches
                                                                                                                                                                                                                                                    Query Match
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                                                                                                                 250 TCTGAACTCGATGGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 300
                                                                                                                                                42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 41)

1 (bases 1 to 41)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Le,M., Lennon,G., Marra,Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Wohldmann,P. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zc10d12.rl Soares parathyroid rumor NbHPA Homo sapiens cDNA clone IMAGE.321911 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 396.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 876 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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    W31998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, R.
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN);, mRNA sequence.
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid_gland; Vector: pT7T3D
(pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco_RI; 1st strand_cDNA was primed_with a Not I -
                                                                                                                                                                                                                                                                                                                                         TTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cct = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:1319302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="parathyroid tumor"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="IMAGE:321911"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:9606"
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/mol_type="mRNA"
                                                                                                                                                                                                                              41.18; 64.78;
                                                                                                                                                                                                         10;
                                                                                                                                                                                                                              Score 38.2; DB Pred. No. 0.63;
    416
                                                                                                                                                                                                           Mismatches
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밁 Ś ORIGIN

Length 411;

Indels

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Gaps

0

linear

EST 20-AUG-1996

Marra, M.,

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ACCESSION
VERSION
KEYWORDS
SOURCE
                                               RESULT
W38764
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AUTHORS
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                          Hominidae; Homo.

(bases 1 to 416)

(chases 1 to 416)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chispes, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hiltman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Hawkins, M., Hiltman, M., Worceba, T., Lacy, M., Le, M., Te, Y., Rifkin, L., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Mardis, E., Gold, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W31998
W31998.1 GI:1313010
EST.
W38764 434 bp mRNA linear EST 15-MAY-1996 zb27a07.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zb96d06.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
IMAGE:320651 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
(HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                    41.1%;
ilarity 64.7%;
Conservative 1
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Location/Qualifiers
                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                              Score 38.2; DB 8;
Pred. No. 0.63;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                        Length 416;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                              0;
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
COMMENT
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VERSION
KEYWORDS
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W56235
LOCUS
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Best Local S
Matches 33
                                                                                                                                                                                                                                                      42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

TMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.REGA+ET

High quality sequence stop: 253.

Location/Qualifiers
          W56235
W56235.1
EST.
                                                                                        W56235
2C01e11.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone image:321068 5' similar to gb:V00597 parathyroID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMAGE:304788 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR (HUMAN);, mRNA sequence. W39764 W39764.1 GI:1320471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hiller,L., Clark,N., Dubuque,T., Le,M., Lennon,G., Marra,M. Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Parsonskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                              Similarity 64.7
33; Conservative
                                                                      (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="GDB:1248198"
/db_xref="taxon:9606"
/clone="IMAGE:304788"
                                                                                                                                                                                                                                                                                                                                                                   41.1%;
                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                 Score 38.2; I
Pred. No. 0.63
0; Mismatches
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.63;
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Marra, M.,

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JOURNAL COMMENT
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AUTHORS
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SOURCE
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W33077
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                                                                                                                                                                                                           DEFINITION
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                                                                                                                                                 ACCESSION
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                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                              42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
                                                                                                                             W33077
W33077.1
                                                                                                                                                                                      W33077

453 bp mRNA linear EST 10-OCT-1990 zc07a12.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE.321598 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo.

1 (bases 1 to 450)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Hultman,M., Kucaba,T., Le,M., Lennon,G., Warra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 865 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
    Hominidae; Homo.
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                 Homo sapiens
                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                    (HUMAN);,
                                                                                                                                                                                                                                                                                                                                     primer: mob.REGA+ET
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTT-3:1, double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_parathyroid_tumor_NbHPA;
/note="Organ: parathyroid_gland; Vector: pT7T3D
(Pharmacia) with a modified_polylinker; Site 1: Not I;
Site_2: Eco RI; 1st strand_cDNA was primed_with a Not I -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                  mRNA sequence.
                                                                                                                                GI:1315062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="IMAGE:321068"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                             41.1%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38.2; DB 8; Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 450;
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                                                                                                                                                                                                                                   EST 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          0
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VERSION
KEYWORDS
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AUTHORS
                                             REFERENCE
AUTHORS
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W56820
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                          241 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 453)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Hominidae; Homo.

1 (bases 1 to 496)

Hillier,L., Clark,N., Dubuque,T., El
Holman,M., Hultman,M., Kucaba,T., Le
Parsons,J., Rifkin,L., Rohlfing,T.,
                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                        zc01a03.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:321004 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                      W56820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 871 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-Merck EST Project
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                     W56820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                W56820.1
                                                                                                                                                                                                                                                     (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Soares parathyroid tumor NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site 1: Not
Site 2: Eco RI; lst strand cDNA was primed with a No
oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                       mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GDB:1259256"
/db_xref="taxon:9606"
                                                                                                                                                                                                                  GI:1358743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="IMAGE:321598"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38.2; DB Pred. No. 0.63; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                    496 bp
                          Elliston, K., Hawkins, M.,
Le, M., Lennon, G., Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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not I;

EST 10-OCT-1996

<u>,,</u>

Gaps

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REFERENCE
AUTHORS
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SOURCE
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W52945
LOCUS
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VERSION
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Matches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                             219
                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
33; Conserv
                                              Hominidae, Homo.

1 (bases 1 to 523)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                               W52945 523 bp
zc03h08.rl Soares parathyroid_tr
IMAGE:321279 5' similar to gb:VV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Whison,R.
Whison,R.
Whison,R.
Wilson RK
Contact: Wilson RK
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                   (HUMAN);, mRNA sequence.
W52945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 858 Std Error: 0.00 Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                 W52945.1 GI:1350379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.1%; Score 38.2; DB 8; ilarity 64.7%; Pred. No. 0.64; Conservative 10; Mismatches 8;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258662"
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                                                                                                                                                                                                                                                                                               old tumor Nbhpa Homo sapiens cDNA clone
gb: V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                     mRNA
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                                                                                    ,G., Marra,M.,
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Best Local Similarity
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                                                                                                      Hominidae; Homo.

1 (bases 1 to 536)

1 (bases 1 to 536)

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hiller, L., Clark, N., Kucaba, T., Le, M., Lennon, G., Marra, M. Holman, M., Hultman, M., Kucaba, T., Le, M., Tan, F., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                   W19765
zb39c03.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone
IMAGE:305956 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                      The WashU-Merck EST Project
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                   (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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8;

0

Gaps

0

Louis,

3

63108

Marra, M.,

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Contact: Wilson RK
Washington University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 702 Std Error: 0.00
Seq primer: mob.REGA-ET
High quality sequence stop: 304.
                                                                                                                                                                                                                                                 quality sequence stop: 304.
Location/Qualifiers
                                                                                            TTTTT-31, double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="GDB:1258937"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
|mol_type="mRNA"
41.1%; Score 38.2; I 64.7%; Pred. No. 0.69 ive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     School of Medicine
vay, Box 8501, St. Louis,
                    .65;
                                    8,
                                      Length 523;
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JOURNAL COMMENT
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W52795
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                                                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 547)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zc02b12.rl Soares parathyroid IMAGE:321119 5' similar to gb
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
                                                                                                                                                                                                     The WashU-Merck EST Project Unpublished (1995)
Contact: Wilson RK
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 651 Std Error: 0.00
                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                     Washington University School of Medicine 44444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMAN);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="parathyroid tumor"
/dev stage="adult"
/lab host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid tumor_NbHPA"
/clone="Organ: parathyroid gland; Vector: pT7T3D
/pharmacia) with a modified polylinker; Site 1: Not 1;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249366"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 bp mRNA linear EST 10-OCT-19)
/roid_tumor_NDHPA Homo sapiens cDNA clone
co gb:V00597 PARATHYROID HORMONE PRECURSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                       Louis, MO
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                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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W56120.1
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                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 576)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W56120 576 bp mRNA linear EST 11-OCT-199 zc56h06.rl Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326363 5' similar to gb:V00597 PARATHYROID HORMONE PRECURSOR
                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810

Fax: 314 286 1810
                                                                                                                                                                                                                                              Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: mob.REGA+ET
                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
INSEC Length: 904 Std Error: 0.00
                   High quality sequence stop: 433
Location/Qualifiers
                                                       Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                              Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMAN);,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:1358009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:321119"
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64.7%;
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AUTHORS
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
W39202
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ORGANISM
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DEFINITION
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 TCTGAACTCGATGGAGAGAGTAGAATGGCTGCGTAAGAAGCTGCAGGATGT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.

1 (bases 1 to 593)

1 (bases 1 to 593)

Hilier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hilier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M.
Holman,M., Hultman,M., Kucaba,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W39202
W39202.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w39202 583 bp mRNA linear EST 15-MAY-1990 zb35h03.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:3056215 similar to gb:V00597 paraTHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 41.1%; Score 38.2; DB 8; Length 576; Similarity 64.7%; Pred. No. 0.66; 33; Conservative 10; Mismatches 8; Indels
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                                                                                                                              primer: mob.REGA+ET
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/mol_type="mRNA"
/db_xref="GDB:1260565"
/db_xref="taxon:9606"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1249031"
/db_xref="taxon:9606"
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/tissue_type="parathyroid tumor"
//dev_stage="dault"
/lab_nost="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Corgan: parathyroid_gland; Vector: pTT3D
/note="Corgan: parathyroid_gland; Vector: pTT3D
/note="Corgan: parathyroid_gland; Vector_stell not I .
Site_2: Eco RI; lst strand cDNA was primed with a Not I -
Oligo(dr) primer
[5:-TGTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."
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Query Match
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                                 ch 41.1%; Score 38.2; DB 1 Similarity 64.7%; Pred. No. 0.66; 33; Conservative 10; Mismatches
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Sequence 132, App
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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APPLICANT: Jung, Eun-Kyung
APPLICANT: Jung, Eun-Kyung
APPLICANT: Dark, Doo-Hong
APPLICANT: Park, Doo-Hong
APPLICANT: Chung, Soo 11
TITLE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE
FILE REPERBNCE: 0136/06626
CURRENT APPLICATION NUMBER: US/99/463,282D
CURRENT PILING DATE: 2000-01-20
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1999-06-05
PRIOR PILING DATE: 1997-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
                                                                                                                                                                                                                                     Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 18519, A
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33, Appl
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Sequence 1970, Ap
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51.1%; Pred. No. 3e-07;
ive 21; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                               US-09-949-016-18519
                                                                                                                                                                                                                                                                                                                                                                                                    JS-09-949-016-66782
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                                                          US-09-108-661-34
US-08-733-446-29
US-08-733-446-30
US-08-733-446-31
US-08-733-446-32
US-08-733-446-32
US-08-733-446-32
US-08-733-446-33
US-08-733-446-33
US-08-733-45-33
US-08-332-45-31-5
US-08-332-45-31-5
US-08-335-231-6
US-08-108-661-5
US-09-108-661-5
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US-08-142-551B-132/C
IS-08-142-551B-132, Application US/08142551B
| Patent No. 5814603 |
| CENERAL INFORMATION: APPLICANT: Oldenburg, Kevin R. APPLICANT: Oldenburg, COMPOUNDS WITH PT |
| TITLE OF INVENTION: COMPOUNDS WITH PT |
| TITLE OF INVENTION: RECOMBINANT DNA V |
| WUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-463-282D-26; Sequence 26, Application US/09463282D Patent No. 6500647; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 51.19
Matches 47; Conservative
TYPE: DNA
ORGANISM: Homo sapiens
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26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGSTAAACACCTGAACTCCCTCGAGCGTG 85
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49.7%; Score 46.2; DB 2; Length 141;
Best Local Similarity 51.6%; Pred. No. 4.8e-05;
Matches 47; Conservative 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08468275
Sequence 5, Application US/08468275
Sequence 5, Application US/08468275
GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDEBRUNG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
ITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950. PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: CALLFORNIA
COUNTRY: CALLFORNIA
COUNTRY: CALLFORNIA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: COMPUTER: Floppy disk
COMPUTER: Determine PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,275
FILING DATE: 06-JUN 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 03660-0002; ARC-2349
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US/08/468,275
[TILING DATE: 06-JUN 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 496-8150
ITELEPHONE: (415) 496-8150
ITELEPHONE: (415) 496-8150
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TENGTH: 141 base pairs
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TELEFAX: (415) 496-8048
INFORMATION FOR SEQ ID NO:
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25
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LOCATION: 7..138
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STREET: 950 ...
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ALTFORNI
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; LOCATION:
US-08-468-275-3
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US-08-468-275-5/c
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; Sequence 3, Application US/08468275
; Sequence 3, Application US/08468275
; Patent No. 5747453
; GENERAL INFORMATION;
; APPLICANT: HOLLADAY, LESLIE A.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: 950 PAGE MILL ROAD
; CITY: PALO ALIPORNIA
; STATE:
; STATE:
; CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.0%; Score 48.4; DB 2; Length 74; Best Local Similarity 74.0%; Pred. No. 8.9e-06; Matches 37; Conservative 12; Mismatches 1; Indels
                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Bloppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Bloppy disk

COMPUTER: IBM PC compatible

APPLICATION NUMBER: US/08/142,551B

FILING APPLICATION NUMBER: US/08/142,551B

FILING DATE: 14-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/898,219

FILING DATE: 12-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/965,677

FILING DATE: 22-OCT-1992

APPLICATION NUMBER: US 07/965,677

FILING DATE: 22-OCT-1992

APPLICATION NUMBER: US 07/965,677

FILING DATE: 22-OCT-1992

APPLICATION NUMBER: 30,113

REFERENCE/DOCKET NUMBER: 000324-010

TELEPHONIS: (415) 854-7400

TELEPHONIS: (415) 854-8275

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE: FRANCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CALIFORNIA
COUNTY: USA
ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
        CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Sw
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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26 CCGTTTCCGAAATCCAGCTGCTGCACAACCTGGGTAAACACCTGAACTCCCTCGAGCGTG 85
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                                                                                                                                                                                                                                                                                                                                                                                                      US-09-007-466-5/c

Sequence 5, Application US/09007466

Patent No. 6313092

GENERAL INFORMATION:

APPLICANT: HOLLADAY, LESLIE A.

APPLICANT: OLDENBURG, KEVIN R.

TITLE OF INVENTION: METHOD FOR INCREASING THE

TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PAPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/468,275

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: MILLER, D. BYRON

REGISTRATION NUMBER: 30,661

REFRENCE/DOCKET NUMBER: 0360-0002; ARC-2349

TELECOMUNICATION INFORMATION:

TELEPHONE: (415) 496-8150

TELEPHONE: (415) 496-8168

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 141 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.6%; Preq. nv.
Marches 47; Conservative 16; Mismatches
47; Conservative 16; Mismatches
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Patent No. 6333189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
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ZIP: 94303-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 141 base pairs
nucleic acid
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
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   Matches
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SEQUENCE 3, Application US/09007466

Patent No. 6313092

GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESLIE A.
APPLICANT: OLDENBURG, KEVIN R.
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94301-0802
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
BELLCATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
BELLCATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
COMPUTER: USA
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                                                                                                                                                                                                                                      49.7%; Score 46.2; DB 2; Length 141; 51.6%; Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                             28; Indels
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,275
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INPORMATION:
NAME: MILLER, D. BYRON
REGISTRATION NUMBER: 30,661
REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10 496-8150
TELEPAX: (415) 496-8150
TELEPAX: (415) 496-8168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S6 TIGAATGGCTGCGTAAAAAACTGCAGGACGT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.7%;
51.6%;
                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.6%;
Matches 47; Conservative 1
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
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                                                                                                          linear
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Best Local Similarity
                                                                                                                               , MOLECULE TYPE:
US-08-468-275-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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, LOCATION:
US-09-007-466-3
                                                                                                       TOPOLOGY:
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US-09-007-466-3
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Indels

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56 TTGAATGGCTGCGTAAAAACTGCAGGACGT 26
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APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-142-551B-8
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GENERAL INFORMATION:
APPLICANT: HOLLADAY, LESILE A.
APPLICANT: OLDENBUGG, KEVIN R.
TITLE OF INVENTION: METHOD FOR INCREASING THE
TITLE OF INVENTION: BLECTROTRANSPORT FLUX OF POLYPEPTIDES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALZA CORPORATION
STREET: 950 PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
CONTYRY: USA
CONPUTER: BALO ALTO
STATE: PALO ALTO
STATE: PAPLO ALTO
COMPUTER: BEADALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC. compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
COMPUTER: DatentIn Release #1.0, Version #1.30
COMPUTER: DATE: 20-NOV-1997
CLASSIFICATION NUMBER: US/08/952,980B
ATTORNEY/AGENT INFORMATION:
RESISTATION NUMBER: 30,661
REPERENCE/DOCKET NUMBER: 2349 CIP 1
TELEPHONE: (650) 496-8048
INPORMATION POR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDSS: SAIRGE
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49.7%; Score 46.2; DB 3; Length 141;
Best Local Similarity 51.6%; Pred. No. 4.88-05;
Matches 47; Conservative 16; Mismatches 28; Indels (
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86 TTGAATGGCTGCGTAAAAAACTGCAGGACGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: mat_peptide
LOCATION: 25
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LOCATION: 7..138
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US-08-952-980B-3
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2 CUGUTUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCGUCAGAACUCCAUGGAACGUG 61
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; Sequence 8, Application US/08142551B
; Patent No. 5814603
; GENERALI INFORMATION:
; APPLICANT: Oldeburg, Kevin R.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burnes, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 49.7%; Score 46.2; DB 3; Length 141; Best Local Similarity 51.6%; Pred. No. 4.8e-05; Matches 47; Conservative 16; Mismatches 28; Indels
ZIP: 94303-0802

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CONTUREN: PatentIn Release #1.0, Version #1.30
SOFTWAREN PELICATION DATA:
PPLIANG DATE: 20-NOV-1997
CILASSITCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, D. BYRON
SEGISTIANTION NUMBER: 30,661
FRIEFRENCE/COCKET NUMBER: 2349 CIP 1
TELEPHONE: (650) 496-8150
TELEPAX: (650) 496-816
TELEPAX: (650) 496-8150
TELEPAX: (650) 496-816
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MEDIUM TYBE: Floppy disk
MEDIUM TYBE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,677
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DESCRIPTION:
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FACELIA NO. 52004;
FACELIA NO. 52004;
APPLICANT: Jung, Eun-Kyung
APPLICANT: Jung, Eun-Kyung
APPLICANT: Doo-Hong
FALE OF INVENTION: RECOMBINANT EXPRESSION VECTOR OF HUMAN PARATHYROID HORMONE
FILE REPERBENCE: 0136/06526
CURRENT APPLICATION NUMBER: 0200-01-20
FRIOR FILING DATE: 1998-06-05
FRIOR FILING DATE: 1998-06-05
FRIOR FILING DATE: 1997-07-07
NUMBER OF SEQ ID NOS: 26
SEQ ID NOS: 26
LENGTH: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encodes the leader peptide sequence that serves to direct the protein into inclusion bodies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 49.7%; Score 46.2; DB 2; Length 207; Similarity 51.6%; Pred. No. 5.3e-05; 47; Conservative 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encodes the protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGU 92
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; Sequence 5, Application US/09463282D
; Patent No. 6500647
                             ATTOKNATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 0003;
TELECOMMUNICATION INFORMATION:
TELEPAK: (415) 854-8275
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
LOCATION: 70..Ī74
OTHER INFORMATION: pepti
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NAME/KEY: misc feature
LOCATION: 175. 207
OTHER INFORMATION: /note
OTHER INFORMATION: havin;
OTHER INFORMATION: purif
US-08-142-551B-8
FILING DATE: 22-OCT-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: 1..51 OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-463-282D-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: OTHER INFORMATION:
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Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                  LOCATION:
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US-10-340-484-14

Sequence 14, Application US/10340484

Sequence 14, Application US/10340484

Sequence 14, Application US/10340484

GENERAL INFORMATION:
TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
TITLE OF INVENTION: Drugs
FILE REFERENCE: 25200-501

FILE REFERENCE: 2003-10-10

CURRENT FAPLICATION NUMBER: US/10/340,484

CURRENT FILING DATE: 2003-10-10

PRIOR APPLICATION NUMBER: 60/347,215
                                                                                             Gaps
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GENERAL INFORMATION:

APPLICANT: KOPETZKI, ETHARG

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

STREPTAVIDIN FUSION PROTEINS

NUMBER OF SEQUENCES:

ADDRESSBEE: ARENT FOX KINTNER PLOTKIN & KAHN

STREET: 1050 CONNECTICUT AVENUE, NW, SUITE 600

CITY: Washington

STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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    Length 45;
                                                                                                                                                                                  Length 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTRY: USA
ZIP: 2018-3339
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,738A
PTING DATE: UNMBER: DC7/EP 96/04850
FTLING DATE: 11-NOV-11996
ATORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
NAME: Berman, Richard J.
NAME: Berman, Richard J.
NAME: REGISTRATION NUMBER: 39,107
REGISTRATION NUMBER: 39,107
REGISTRATION NUMBER: PLOB341-08035
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TENTOR TO THE PROBATION:
NAME TO THE PROBATION:
NA
Query Match

46.7%; Score 43.4; DB 3;
Best Local Similarity 73.3%; Pred. No. 0.00027;
Matches 33; Conservative 11; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.2%; Score 43; DB 3; I Best Local Similarity 76.7%; Pred. No. 0.00039; Matches 33; Conservative 10; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other nucleic acid
/desc = "synthetic
oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09068738A
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TYPE: nucleic acid
STRANDEDNESS: single
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Gaps

0

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42 ucucaacuccauggaacguguugaauggcugcguaaaaaacugcaggacgu 92
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                                                                                                                                                                                             42 UCUGAACUCCAUGGAACGUGUUGAAUGGCUGCGUAAAAAACUGCAGGACGU 92
                                                                                                                                                                                                                                 24 TTTGAACTCCATGGAGCGTGTAGAATGGCTGCGTAAGAAGTTGCAGGATGT 74
                                                                                                                                                                                                                                                                                                                           RESULT 14

CAS 08-733-446-61

Sequence 61, Application US/08733446

Patent No. 5856138

GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS AND TITLE OF INVENTION: PRODUCTION THEREOF

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
ADDRESSEE: DATE G. COLLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN

STREET: DATE G. COLLIN, DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN

STREET: DATE G. COLLIN, DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                             Query Match
42.8%; Score 39.8; DB 2; Length 234;
Best Local Similarity 64.7%; Pred. No. 0.0049;
Matches 33; Conservative 11; Mismatches 7; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 4,6
IDENTIFICATION METHOD: E
   ; IDENTIFICATION METHOD:
US-08-733-446-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
COUNTRY: US
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LOCATION: 1..234
NAME/KEY: mutation
LOCATION: 4,6
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US-08-733-446-19

US-08-733-446-19

US-08-733-446-19

SEQUENCE 19, Application US/08733446

Patent No. 5865138

GENERAL INFORMATION:
HUMAN PARATHYROID HORMONE MUTEINS AND TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS AND TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS AND TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTEINS SEE: CORMINES: 6

CORRESPONDENCE ADDRESS: 62

ADDRESSEE: CUSHAAN
STREE: 130 Water Street
STATE: Massachusetts
COUNTRY: US

COUNTRY: US

COUNTRY: US

COUNTRY: US

COUNTRY: IBM PC COMPATABLE
COMPUTER: READABLE FORM:
MEDIUM TYPE: FLOOPY disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: PLOOPY disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: US/08/MS-DS

SOFTWARE: PAREINION DATA:
APPLICATION NUMBER: US/08/133,446

FLLING DATE:
APPLICATION NUMBER: US/08/133,446

FLLING DATE:
FLLING DAT
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42.8%; Score 39.8; DB 3; Length 102;
Best Local Similarity 64.7%; Pred. No. 0.0041;
Matches 33; Conservative 11; Mismatches 7; Indels
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PRIOR FILING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01
PRIOR PLING DATE: 2002-01
PRIOR PRILING DATE: 2002-01
PRIOR PRILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/379,125
PRIOR APPLICATION NUMBER: 60/379,125
PRIOR SEQ ID NOST: 27
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 14
LENGTH: 102
                                                                                                                                                                                                                                                                                                       TYPE: DNA
; ORGANISM: Homo sapiens
US-10-340-484-14
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RESULT 15
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Sequence 20, Application US/08733446
Sequence 20, Application US/08733446
Sequence 20, Application US/08733446
Sequence 20, Application US/0873346
Sequence 20, Application US/0873346
Sequence 20, Application US/087370
TITLE OF INVENTION: PRODUCTION THEREOF
TITLE OF INVENTION: PRODUCTION THEREOF
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
COMPTTER READBLE FORM:
MAINTER READBLE FORM:
COMPTTER READBLE FORM:
MAINTER READBLE FORM:
MAINTER READBLE FORM:
ADDRESSEE: US/08/402,970
FILING DATE: 18-CT-196
CLASSITICATION NUMBER: US/09/402,970
FILING DATE: NUMBER: US/09/402,970
FILING DATE: NUMBER: US/09/402,970
FILING DATE: NUMBER: GEORGE W.
REFERENCE/DOCKET NUMBER: 4002
FILING DATE: NUMBER: GEORGE W.
REFERENCE/DOCKET NUMBER: 4002
FILING DATE: ADDRESSEE: GOUDLE
TRELEMAN: (417)523-440
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27 TTTGAACTCCATGGAGCGTGTAGAATGGCTGCGTAAGAAGTTGCAGGATGT 77

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Search completed: November 24, 2005, 01:34:15 Job time: 74.6667 secs

Oden Mole Bood sint

Fri Nov 25 10:36:39 2005

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November 23, 2005, 23:59:22 ; Search time 412.667 Seconds (without alignments) 1863.616 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2.6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
3: /cgn2.6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2.6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2.6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2.6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2.6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2.6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
9: /cgn2.6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
9: /cgn2.6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2.6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-407-078-14
US-10-997-078-14
US-10-997-078-60
US-10-997-078-141
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US-10-997-078-133
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Maximum Match 100%
Listing first 45 summaries
                                                             using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                             Run on:
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APPLICANT: Walker, Kenneth
APPLICANT: Walker, Kenneth
APPLICANT: Xiong, Fei
TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the SeruFILE REFERENCE: A-813A
CURRENT APPLICATION NUMBER: US/10/407,078
FRICE APPLICATION NUMBER: A-813
PRIOR APPLICATION NUMBER: A-813
PRIOR FILING DATE: 2002-04-04

Sequence 14, Application US/10407078; Publication No. US20030195154A1; GENERAL INFORMATION:

RESULT 2 US-10-407-078-14

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2 CUGUIUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUCGGAACUCCAUGGAACGUG

62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93 

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1ce 14, Appl 1ce 51, Appl 1ce 1, Appl 1ce 1, Appli 1ce 1, Appli 1ce 2, Appli 1ce 24, Appl 1ce 25, Appl 1ce 25, Appl 1ce 52, Appl 1ce 52, Appl 1ce 64, Appl 1ce	ns to Increase the Serül
sednence seane sea	Protein Fusion . Length 489;
US-10-340-484-14 US-09-879-257A-51 US-09-879-257A-52 US-10-35-091-1 US-10-35-091-1 US-10-35-091-3 US-10-35-091-7 US-10-359-091-7 US-10-359-091-7 US-10-75-204-25 US-10-775-204-51 US-10-775-204-51 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61 US-10-775-204-61	IGNMENTS  retin Peptide/ 17,109  e 52; DB 6; No. 2.6e-07; imarches
1002 1002 1002 1002 1002 1002 1002 1002	tion US/ 03019105 C. Kenneth Fei Use of 13 13 13 13 13 13 13 13 14 13 14 13 14 13 14 14 14 14 14 14 14 14 14 14 14 14 14
. 4444444444444444444 . KNUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU	SULT 1  -10-117-109-14  Sequence 14, Application US, Publication Wo. US2003019106  GENERAL INFORMATION: APPLICANT: Amgen Inc. APPLICANT: Xiong, Fei TITLE OF INVENTION: Use of FILE REFERENCE: A-BILL REFERENCE: A
	RESULT 1 US-10-117-109-14 ; Sequence 14, A ; Sequence 14, A ; Deblication No ; GENERAL INFORM APPLICANT: Am APPLICANT: Am APPLICANT: X TITLE OF INVE ; TILE REFERENC ; CURRENT FILIN CURRENT FILIN CURRENT FILIN ; CURRENT MAD ; ORGANISM: HO US-10-117-109-14
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-10-117. Sequence Sequence GENERAL APPLICA APPLICA TITLE (

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Sequence 33, Application US/10997700

Publication No. US20050239172A1

GENERAL INFORMATION:

APPLICANT: Wagner, F.

APPLICANT: Wagner, F.

APPLICANT: Holmquist, B.

APPLICANT: Holmquist, B.

APPLICANT: Holmquist, B.

TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic CURRENT APPLICANTON NUMBER: US/10/997, 700

CURRENT PILING DATE: 2004-11-24

PRICR APPLICATION NUMBER: US 60/383,212

PRICR APPLICATION NUMBER: US 60/383,212

PRICR PRICR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 93

SOFTWARE: RastSEQ for Windows Version 4.0

LENGTH 10.9
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| Publication No. US20050221444A1
| GENERAL INFORMATION:
| APPLICANT: Wagner, F. APPLICANT: Wagner, E. APPLICANT: Holmquist, B. APPLICANT: Restoragen, Inc.
| APPLICANT: Restoragen, Inc.
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54.2%; Score 50.4; DB 9; Length 102;
Best Local Similarity 52.2%; Pred. No. 6.2e-07;
Matches 48; Conservative 18; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.2%; Score 50.4; DB 9; Length 102; Best Local Similarity 52.2%; Pred. No. 6.2e-07; Matches 48; Conservative 18; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 TTGAATGGCTGCGTAAAAACTGCAGGACGTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH: 102
                                                                                                                                                                  ), OTHER INFORMATION: PTH(1-34).
US-10-997-078-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: PTH(1-34).
US-10-997-700-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                            TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-10-997-700-33
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APPLICANT: Wagner, F.
APPLICANT: Peng, L.
APPLICANT: Xia, U.
APPLICANT: No. V.
APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
APPLICANTON: Methods and DNA Constructs for High Yield Production of Polypepti TITLE OF INVENTION: Wethods and DNA Constructs for High Yield Production of Polypepti CURRENT APPLICATION NUMBER: 2010/997,078
CURRENT PILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2002-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-407-078-43
US-10-407-078-43
Sequence 43, Application US/10407078
Publication No. US20030195154A1
Sequence 43, Application US20030195154A1
Publication No. US20030195154A1
GENERAL INFORMATION:
APPLICANT: Xiong, Fei
TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the Seru;
FILLE REFERENCE: A-813A
CURRENT APPLICATION NUMBER: US/10/407,078
FRIOR APPLICATION NUMBER: A-813
FRIOR PILING DATE: 2003-04-03
FRIOR PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 43
LENGTH: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                          2 CUGUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUCUGAACUCCAUGGAACGUG 61
                                                                                                                                                                                                                                                                                                                      64
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Best Local Similarity 51.1%; Pred. No. 2.6e-07;
Matches 47; Conservative 20; Mismatches 25; Indels
                                                                                                                                                                                           Query Match 55.9%; Score 52; DB 6; Length 489 Best Local Similarity 51.1%; Pred. No. 2.6e-07; Matches 47; Conservative 20; Mismatches 25; Indels Matches 47; Conservative 20; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               65 TTGAATGGCTGCGTAAGAACTGCAGGACGTT 96
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US-10-997-078-60
Sequence 60, Application US/10997078
Publication No. US20050221444A1
GENERAL INFORMATION:
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; LENGTH: 489
                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-407-078-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-407-078-43
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APPLICATION RESPONSED. Inc.
TITLE OP INVENTION: Methods and DNA Constructs for High Yield Production of Polypeptic FILE REPERENCE: 1627.010081
CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wagner, F.
APPLICANT: Wagner, F.
APPLICANT: Wagner, L.
APPLICANT: Peng, L.
APPLICANT: Applicant Xia, U.
APPLICANT: Holmquist, B.
APPLICANT: Restoragen, Inc.
ITILE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti FILE REFERENCE: 1627, 010051.
FILE REFERENCE: 1627, 010051.
FILE REFERENCE: 1627, 010051.
FILE REFERENCE: 1627, 010051.
FILE REFERENCE: 1004-11-34
CURRENT APPLICATION NUMBER: 2004-11-34
PRIOR FILING DATE: 2003-05-23
PRIOR FILING DATE: 2003-05-24
PRIOR FILING DATE: 2003-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE FRASEEQ for Windows Version 4.0
SEQ ID NO 62.
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54.2%; Score 50.4; DB 9; Length 252;
Best Local Similarity 52.2%; Pred. No. 7.6e-07;
Matches 48; Conservative 18; Mismatches 26; Indelb (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.2%; Score 50.4; DB 9; 1
Best Local Similarity 52.2%; Pred. No. 6.4e-07;
Matches 48; Conservative 18; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ), OTHER INFORMATION: A synthetic PTH sequence. US-10-997-078-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 62, Application US/10997078
; Publication No. US20050221444A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: PTH(1-84).
US-10-997-078-62
Peng, L.
Xia, U.
Holmquist, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-10-997-078-62
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; Sequence 34, Application No. US20050239172A1
; Sequence 34, Application No. US20050239172A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, F.
; APPLICANT: Wagner, F.
; APPLICANT: Xia, U.
; APPLICANT: Holmquist, B.
; TITLE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti; PILE REFERENCE: 1627.009US1
; CURRENT APPLICATION NUMBER: US/10/997,700
; CURRENT APPLICATION NUMBER: US 60/383,212
; PRIOR PLING DATE: 2002-05-24
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 93
; SOFTHARE: FeatSEQ for Windows Version 4.0
; SEQ ID NO 34
; LEWIGTH: 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.2%; Score 50.4; DB 9; 52.2%; Pred. No. 6.3e-07; tive 18; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
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CURRENT APPLICATION NUMBER: US/10/997,078
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: PCT/US03/16643
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/383,370
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FSSESEQ for Windows Version 4.0
SEQ ID NO 61
LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 141, Application US/10997078; Publication No. US20050221444A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: PTH(1-37).
US-10-997-078-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: PTH(1-37)
US-10-997-700-34
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Best Local Similarity 52.27
Marches 48; Conservative
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Best Local Similarity 52.2
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                   ORGANISM: Unknown
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                                                                                                                                                                                                                                TYPE: DNA
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54.2%; Score 50.4; DB 9; Length 276;
Best Local Similarity 52.2%; Pred. No. 7.8e-07;
Matches 48; Conservative 18; Mismatches 26; Indels (
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US-10-997-622-3
isequence 3, Application US/10997822
isequence 3, Application US/10997822
isequence 3, Application No. US20050227314A1
isemEREAL INFORMATION.
is APPLICANT: Holmquist, B.
is APPLICANT: Genealk, X.
is APPLICANT: Genealk, X.
is APPLICANT: Cayer, R.
itILE OF INVENTION: POLYPEPTIDE CLEAVAGE PROCESS FILE REFRENCE: 1627.011US1
is CURRENT APPLICATION NUMBER: US/10/997,822
CURRENT PILING DATE: 2003-05-23
is PRIOR APPLICATION NUMBER: DGT/WS03/16647
is PRIOR APPLICATION NUMBER: US 60/383,484
is PRIOR APPLICATION NUMBER: US 60/383,484
is PRIOR APPLICATION UNMBER: US 60/383,484
is PRIOR ETLING DATE: 2002-05-24
is SOFTWARE: FastSEQ for Windows Version 4.0
is SEQ ID NO 3
is LENGTH: 276
                                                                                                                                                                         Sequence 18, Application US/10997762
; Publication No. US20050227313A1
GENERAL INFORMATION: US2005027313A1
GENERAL INFORMATION: US2005027313A1
APPLICANT: Serv. Jin Seog.
; APPLICANT: Strydom, Daniel
APPLICANT: Holmquist, Barton
; APPLICANT: Restoragen Inc.
TITLE OF INVENTION: Polypepide Cleavage Process
FILE REFERENCE: 1627.026US1 US/10/997,762
CURRENT APPLICATION NUMBER: US/10/997,762
CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16468
PRIOR FLIING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,488
; RIOR APPLICATION NUMBER: US 60/383,488
; NUMBER OF SEO ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 276
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233 TTGAATGGCTGCGTAAAAACTGCAGGACGTT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 UUGAAUGGCUGCGUAAAAAACUGCAGGACGUU 93
                62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                         65 TTGAATGGCTGCGTAAAAAACTGCAGGACGTT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                    RESULT 10
US-10-997-700-35

Sequence 35, Application US/10997700

Publication No. US20550239172A1

GENERAL INFORMATION:

APPLICANT: Wagner, F.

APPLICANT: Xia, U.

APPLICANT: Aib, U.

APPLICANT: Aib, U.

APPLICANT: TILE OF INVENTION: Methods and DNA Constructs for High Yield Production of Polypepti;

FILE REFERENCE: 1627.009US1

CURRENT APPLICATION NUMBER: US/10/997,700

CURRENT FILING DATE: 2004-11-24

FRIOR PELLING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 93

SOFTWARE: PERSES FREE: Windows Version 4.0

SEQ ID NO 35

LENGTH: 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.2%; Score 50.4; DB 9; Length 252; Best Local Similarity 52.2%; Pred. No. 7.6e-07; Matches 48; Conservative 18; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.2%; Score 50.4; DB 9; Length 264; Best Local Similarity 52.2%; Pred. No. 7.7e-07; Matches 48; Conservative 18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; CTHER INFORMATION: A synthetic pBN121-M-PTH(1-84).
US-10-997-700-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 UUGAAUGGCUGCGUAAAAACUGCAGGACGUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 TTGAATGGCTGCGTAAAAACTGCAGGACGTT 93
62 TIGAAIGGCIGCGIAAAAAACIGCAGGACGII 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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US-10-997-700-35
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ORGANISM: Unknown
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US-10-997-700-89
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ò Вp ò g Dp

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Gaps

; 0

Length 282;

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; TYPE: DNA PATIFICIAL Sequence ; PEATURE: . ORGANISM: Artificial Sequence ; PEATURE: ; OTHER INFORMATION: A synthetic sequence for the T7tagVg-PTH(1-34) cassette. US-10-997-078-133
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

54.2%; Score 50.4; DB 9; Length 2

Best Local Similarity 52.2%; Pred. No. 7.8e-07;

Matches 48; Conservative 18; Mismatches 26; Indels
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Sequence 133, Application US/10997078

Publication No. US20050221444A1

GENERAL INFORMATION:

APPLICANT: Wagner, F.

APPLICANT: Wagner, F.

APPLICANT: APPLICANT: Manager, Inc.

APPLICANT: Ala, U.

BRIOR PILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 148

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 133

FENCH: Ala, U.

FE
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CURRENT APPLICATION NUMBER: US/10/997,700
CURRENT FILING DATE: 2004-11-24
PRIOR PELING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 75
LENGTH: 276
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   Query Match 54.2%; Score 50.4; DB 9; Length 276; Best Local Similarity 52.2%; Pred. No. 7.8e-07; Matches 48; Conservative 18; Mismatches 26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-997-700-75
; Sequence 75. Application US/10997700
; Publication No. US20050239172A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.2%
Matches 48; Conservative
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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:

November 24, 2005, 01:30:39; Search time 195 Seconds

(without alignments)

70.875 Million cell updates/sec

Perfect score: 93
Sequence: 1 gcuguuuccgaaaucggugg......guaaaaaacugcaggacguu 93
Scoring table: IDBNTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 3205263 segs, 74304013 residues

Total number of hits satisfying chosen parameters: 6410526
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Database : Published\_Applications\_NA\_New:\*

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4: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Sequence 116, App	Sequence 1, Appli	Sequence 3, Appli	Sequence 839, App	Sequence 35, Appl	Sequence 4301, Ap	Sequence 766, App	Sequence 119, App	Sequence 100, App	Sequence 255, App	Sequence 775, App	Sequence 4, Appli		Sequence 4, Appli	Sequence 268, App	Sequence 82, Appl	Sequence 758, App	Sequence 374, App	Sequence 77, Appl	Sequence 19, Appl	Sequence 33, Appl	Sequence 34, Appl	Sequence 621, App
US-10-927-641-116	US-10-509-422-1	US-10-509-422-3	US-10-821-234-839	US-10-131-826A-35	US-10-793-626-4301	US-10-821-234-766	US-10-821-234-119	US-10-467-962B-100	US-10-821-234-255	US-10-821-234-775	US-10-526-731-4	US-10-131-826A-531	US-10-485-517-4	US-10-821-234-268	US-10-467-962B-82	US-10-821-234-758	US-10-802-796-374	US-11-074-176-77	US-11-015-546A-19	US-10-994-820A-33	US-11-013-247A-34	US-10-793-626-621
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28.2	28.2	28.2	28	26.4	25.2	25	24.6	24.4	24.4	24.2	24	23.8	23.8	23.8	23.4	23.4	23	23	23	23	23	22.8
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US-10-812-234-839 Sequence 8 27.1 23.4 31 US-10-131-826A-35 Sequence 2 26.9 1065 1 US-10-821-234-766 Sequence 7	30.3 347 1 US-10-927-641-116 Sequence 1 30.3 3507 1 US-10-509-422-1 Sequence 3 30.3 3704 1 US-10-509-422-3 Sequence 3 30.1 6497 1 US-10-821-234-839 Sequence 3 28.4 3371 1 US-10-131-826A-35 Sequence 3 27.1 2536 1 US-10-793-626-4301 Sequence 7 26.5 2218 1 US-10-821-234-766 Sequence 7 26.5 2218 1 US-10-821-234-119 Sequence 7 26.5 2218 1 US-10-821-234-119	1 28.2 30.3 347 1 US-10-927-641-116 Sequence 1 2 28.2 30.3 3507 1 US-10-509-422-1 Sequence 1 3 28.2 30.3 3704 1 US-10-509-422-3 Sequence 2 8 30.1 6497 1 US-10-509-422-3 Sequence 3 5 26.4 28.4 3371 1 US-10-131-826A-35 Sequence 6 2 5.2 27.1 2536 1 US-10-131-826A-35 Sequence 7 7 2 5 26.9 1065 1 US-10-793-626-4301 Sequence 7 7 2 5 22.18 1 US-10-812-234-766 Sequence 1 US-10-812-234-109 Sequence 1 US-10-812-234-100 Sequence 1 US-10-812-100	2 28.2 30.3 357 1 US-10-927-641-116 Sequence 116, 2 28.2 30.3 3507 1 US-10-509-422-1 Sequence 1, Ag 28.2 30.3 3704 1 US-10-509-422-3 Sequence 3, Ag 4 28.3 30.1 6497 1 US-10-509-432-3 Sequence 3, Ag 5 26.4 28.4 3771 US-10-131-8268-35 Sequence 35, Ag 1 US-10-812-234-76 Sequence 4301, 2 2 26.9 1065 1 US-10-821-234-76 Sequence 766, 2 2 2 2 2 2 2 2 1 US-10-821-234-119 Sequence 766, 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1 28.2 30.3 3507 1 US-10-927-641-116 Sequence 1 2 2 2 3 3 3 5 0 7 1 US-10-509-422-1 Sequence 3 3 2 2 3 0.3 3 704 1 US-10-509-422-3 Sequence 3 3 2 2 3 0.3 3 704 1 US-10-509-422-3 Sequence 5 5 2 4 2 8 4 3 7 1 US-10-811-826A-35 Sequence 6 2 5 2 2 7 1 2 5 3 6 1 US-10-131-826A-35 Sequence 6 2 5 2 2 7 1 2 5 3 6 1 US-10-131-826A-35 Sequence 7 2 5 6 5 2 18 1 US-10-821-234-119 Sequence 1 US-10-821-234-119 Sequence 1 US-10-821-234-119 Sequence 1 US-10-821-234-125 Sequence 1 US-10-821-234-255 Sequence 1 US-10-821-234-255 Sequence 2 1 2 2 6 2 3 3 3 3 1 US-10-821-234-255 Sequence 2 2 6 2 6 3 1 US-10-821-234-255 Sequence 7 Sequence 7 2 5 6 2 6 2 6 2 6 2 6 2 6 2 6 2 6 2 6 2	2 8.2 30.3 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Sequence 1, Ag 28.2 30.3 3704 1 US-10-509-422-3 Sequence 3, Ag 28.2 30.3 3704 1 US-10-131-826A-35 Sequence 35, Ag 26.2 27.1 2536 1 US-10-131-826A-35 Sequence 4301, 25.2 27.1 2536 1 US-10-793-626-4301 Sequence 4301, 24.4 26.2 2043 1 US-10-821-234-119 Sequence 110, 24.4 26.2 2043 1 US-10-821-234-119 Sequence 100, 24.4 26.2 3083 1 US-10-821-234-125 Sequence 100, 24.4 26.2 3083 1 US-10-821-234-255 Sequence 775, 12 24 25.8 2748 1 US-10-526-731-4 Sequence 531, 23.8 25.6 1150 1 US-10-131-826A-531 Sequence 5.31, 23.8 25.6 5690 1 US-10-821-234-268 Sequence 5.8 31, 23.8 25.6 4770 1 US-10-821-234-268 Sequence 26.8 31, 23.8 25.6 4770 1 US-10-821-234-268 Sequence 6.2 8, 23.4 25.2 4770 1 US-10-821-234-268 Sequence 82, 8	2 8.2 30.3 347 1 US-10-927-641-116 Sequence 116, 28.2 30.3 3507 1 US-10-509-422-1 Sequence 1, Mg 2 8.2 30.3 3504 1 US-10-509-422-3 Sequence 1, Mg 2 8.2 30.3 3704 1 US-10-6927-631 Sequence 3, Mg 6 25.2 27.1 5536 1 US-10-131-826A-35 Sequence 35, Mg 6 25.2 27.1 5536 1 US-10-131-826A-35 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3507 1 US-10-509-422-1 Sequence 1, Ag 28.2 30.3 3504 1 US-10-509-422-3 Sequence 1, Ag 28.2 30.3 3704 1 US-10-509-422-3 Sequence 3, Ag 28.2 30.1 6497 1 US-10-131-826A-35 Sequence 839 Sequence 839 Sequence 839 Sequence 839 Sequence 8301, 25.2 27.1 2536 1 US-10-79-626-4301 Sequence 4301, 25.2 27.1 2536 1 US-10-821-234-119 Sequence 109, 24.4 26.2 2043 1 US-10-821-234-125 Sequence 775, 25.9 115 23.8 25.6 1150 1 US-10-821-234-25 Sequence 6.1 Mg 13 23.8 25.6 14770 1 US-10-821-234-26 Sequence 263, 116 23.4 25.2 477 1 US-10-821-234-26 Sequence 82, Requence 82, Requenc	2 8.2 30.3 347 1 US-10-927-641-116 Sequence 116, 28.2 30.3 3507 1 US-10-509-422-1 Sequence 1, Mg 28.2 30.3 3504 1 US-10-509-422-3 Sequence 1, Mg 28.2 30.3 3704 1 US-10-6927-631 Sequence 3, Mg 5.2 27.1 53.4 1 US-10-131-826A-35 Sequence 35, Mg 6.2 27.1 53.6 1 US-10-131-826A-35 Sequence 35, Mg 24.6 26.5 2218 1 US-10-821-234-766 Sequence 119, 24.4 26.2 2043 1 US-10-821-234-719 Sequence 110, 24.4 26.2 3043 1 US-10-821-234-119 Sequence 110, 24.4 26.2 3043 1 US-10-821-234-255 Sequence 110, 24.4 26.2 3043 1 US-10-821-234-255 Sequence 255, Ill 24.5 8.7 48 1 US-10-821-234-256 Sequence 255, Ill 23.8 25.6 1150 1 US-10-131-826A-531 Sequence 4, Mg 12.3 25.6 14770 1 US-10-485-517-4 Sequence 25.8 17.8 17.2 1.8 25.2 7008 1 US-10-821-234-268 Sequence 25.8 17.8 25.2 7008 1 US-10-821-234-268 Sequence 758, Ill 23.4 25.2 7008 1 US-10-821-234-758 Sequence 758, Ill 23.4 25.2 7008 1 US-10-821-234-78 Sequence 374, Ill 23.4 25.2 7008 1 US-10-821-234-78 Sequence 377, Ill 23.4 25.2 7008 1 US-10-821-234-78 Sequence 19, Mg 23.2 4.7 1852 7 US-10-821-234-78 Sequence 19, Mg 23.4 7 1852 7 US-10-821-234-79 Sequence 19, Mg 23.2 4.7 1852 7 US-11-61-65-546A-19 Sequence 19, Mg 23.2 4.7 1852 7 US-11-61-65-546A-19 Sequence 19, Mg 24.7 1852 7 US-11-61-61-61-61-61-61-61-61-61-61-61-61-	28.2 30.3 347 1 US-10-927-641-116 Sequence 116, 28.2 30.3 3504 1 US-10-509-422-1 Sequence 1, Ag 28.2 30.3 3704 1 US-10-509-422-3 Sequence 1, Ag 28.2 30.3 3704 1 US-10-509-422-3 Sequence 13, Ag 26.4 28.4 3371 1 US-10-131-826A-35 Sequence 35, Ag 26.4 28.4 3371 1 US-10-131-826A-35 Sequence 35, Ag 24.6 26.5 2218 1 US-10-821-234-76 Sequence 116, Sequence 116, 24.4 26.2 2043 1 US-10-821-234-119 Sequence 110, 24.4 26.2 3893 1 US-10-821-234-125 Sequence 110, 24.4 26.2 3893 1 US-10-821-234-255 Sequence 110, 24.4 26.2 3893 1 US-10-821-234-255 Sequence 255, 11 24.2 26.9 963 1 US-10-821-234-255 Sequence 255, 12 23.8 25.6 1150 1 US-10-821-234-75 Sequence 268, 14 23.8 25.6 14770 1 US-10-821-234-26 Sequence 268, 16 23.4 25.2 7008 1 US-10-821-234-75 Sequence 268, 17 23.4 25.2 7008 1 US-10-821-234-75 Sequence 374, 17 23.4 25.2 7008 1 US-10-821-234-75 Sequence 374, 18 23 24.7 1849 7 US-11-015-546A-19 Sequence 19, Ag 23 24.7 1849 7 US-11-015-546A-19 Sequence 19, Ag 23 24.7 1849 7 US-11-015-546A-19 Sequence 13, Ag 24, 1956 1 US-11-015-546A-19 Sequence 33, Ag 24.7 1956 1 US-11-015-246-33, Ag 24.7 1956 1 US-11-015-246-34 33, Ag 24.7 1956 1 US-11-015-246-34 33, Ag 24.7 1956 1 US-11-015-246-34 33, Ag 24.7 1956 1 US-11-015-	28.2 30.3 347 1 US-10-927-641-116 Sequence 116, 28.2 30.3 3507 1 US-10-509-422-1 Sequence 1, Ag 28.2 30.3 3704 1 US-10-509-422-3 Sequence 1, Ag 28.2 30.3 3704 1 US-10-509-422-3 Sequence 13, Ag 28.2 30.1 6497 1 US-10-131-826A-35 Sequence 839, 25.2 27.1 2536 1 US-10-131-826A-35 Sequence 4301, 25.2 27.1 2536 1 US-10-793-626-4301 Sequence 4301, 24.4 26.2 2043 1 US-10-821-234-119 Sequence 110, 24.4 26.2 2043 1 US-10-821-234-119 Sequence 110, 24.4 26.2 2043 1 US-10-821-234-125 Sequence 110, 24.4 26.2 2043 1 US-10-821-234-255 Sequence 255, 112 22.6 3893 1 US-10-821-234-255 Sequence 4, Ag 11 24.2 26.0 1 US-10-821-234-25 Sequence 2631, 23.8 25.6 14770 1 US-10-821-234-268 Sequence 2631, 23.8 25.6 14770 1 US-10-821-234-268 Sequence 2631, 23.4 25.2 7008 1 US-10-821-234-268 Sequence 77, 23.4 25.2 7008 1 US-10-821-234-768 Sequence 77, 23.4 25.2 7008 1 US-10-821-234-78 Sequence 77, 23.4 25.2 7008 1 US-10-802-796-374 Sequence 77, 23.4 25.2 7008 1 US-10-802-796-374 Sequence 33, 24.7 1152 7 US-11-074-176-77 Sequence 33, 24.7 1152 7 US-11-013-246A-19 Sequence 33, 24.7 1152 7 US-11-013-247A-34 Sequence 33, 24.7 1152 7 US-11-013-247A-34 Sequence 33, 24.7 1152 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence									
US-11-074-176-353	US-11-074-176-185	US-11-082-389-35	US-11-082-389-33	US-10-793-626-4106	US-10-793-626-4133	US-11-065-943-19	US-11-065-943-21	US-11-065-943-23	US-11-065-943-25	US-11-065-943-27	US-11-065-943-29	US-11-065-943-31	US-11-065-943-33	US-11-065-943-35	US-11-065-943-37	US-10-821-234-47	US-10-839-799-110	US-10-839-799-100	US-10-839-799-101	US-10-839-799-108	US-10-971-560-9
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24.5	24.5	24.5	24.5	24.5	24.5	24.1	24.1	24.1	24.1	24.1	24.1	24.1	24.1	24.1	24.1	24.1	23.9	23.9	23.9	23.9	23.9
22.8	22.8	22.8	22.8	22.8	22.8	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.2	22.2	22.2	22.2	22.2
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

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US-GUBERCE 116, Application US/1097641

Sequence 116, Application US/1097641

SEGNERAL INFORMATION:

APPLICANT: Raid- Stephen

APPLICANT: Raid- Stephen

APPLICANT: Baldero, Clare

APPLICANT: Candero, Marion

APPLICANT: Labham, Annetee

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: MOMBER: US/10/927,641

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: PRIOR 201/00115

PRIOR APPLICATION NUMBER: PRIOR 201/00115

PRIOR APPLICANTON NUMBER: PCT/NZ 01/00116

PRIOR APPLICANTON NUMBER: PCT/NZ 01/0018

PRIOR APPLICANTON NUMBER: US, No. 09/598,401

PRIOR APPLICANTON NUMBER: US, No. 09/276,599

PRIOR APPLICANTON NUMBE
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Sequence 1, Application US/10509422

Publication No. US20050244825A1

General Information No. US20050244825A1

APPLICANT Liou, Simon
ITLLE OF INVENTION: Human BMP2 Inducible Kinases
FILE REFERENCE: 004974 01015

CURRENT APPLICATION NUMBER: US/10/509,422

CURRENT APPLICATION NUMBER: PCT/EP03/080825

PRIOR FILING DATE: 2003-03-20

PRIOR PILING DATE: 2003-03-27

PRIOR APPLICATION NUMBER: US 60/406,936

PRIOR APPLICATION NUMBER: US 60/406,936

PRIOR APPLICATION NUMBER: US 60/406,936

PRIOR PILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US 60/406,936

WUMBER OF SEG ID NOS: 9

SOFTWARE: RestSEQ for Windows Version 4.0
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Best Local Similarity 60.6
Matches 20; Conservative
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, ORGANISM: Homo sapiens
US-10-509-422-1
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; ORGANISM: Homo sapiens
US-10-509-422-3
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LENGTH: 3507
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RESULT 4
US-10-21234-839
US-10-21234-839
Sequence 839, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: LADAL, IVAN

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APPLICANT: WACAGUEDE, COLLIN A.
APPLICANT: WACAGUEDE, COLLIN A.
APPLICANT: ALANGY, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND THE SAME
FILE REFERENCE: P3330RIC128
CURRENT APPLICATION NUMBER: U5/10/131,826A
CURRENT FILING DATE: 000-04-24
RIOR APPLICATION NUMBER: 60/056974
PRIOR PILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056913
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-19
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APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PILING DATE: 2005-04-07
NUMBER: OF SEQ ID NOS: 1704
SOFTWARE: PLEQ Genes Version 1.0
SEQ ID NO 839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-821-234-839
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; ORGANISM: Homo sapiens
US-10-821-234-766
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Sequence 76, Application US/005025514A1

GENERAL INFORMATION:
APPLICANT: Labat, Toan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani
APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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US-10-793-626-4301/C
US-10-793-626-4301/C
Sequence 4301, Application US/10793626
Publication No. US200S0255478A1
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPREBNCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PLING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550 SEQ ID NO 35.
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                                                                                                                                                                                                                                                                                                                    28.4%; Score 26.4; DB 1; Length 3371; 46.7%; Pred. No. 7.6;
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43.5%; Pred. No. 17;
tive 12; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                                                                                                                                                                                                                                                        Query Match 28.4%; Score 26.4; Dr
Best Local Similarity 46.7%; Pred. No. 7.6;
Matches 28; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 43.59
Matches 27; Conservative
                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1658 AA 1657
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LENGTH: 2536
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US-10-214-119/C
Sequence 119, Application US/10821234
Sequence 119, Application No. US20050253114A1
SUBLICATION NO. US20050253114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT PILLORD DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
                                                                                                                                            264 GITICCAIGGCIGGIGGIGGGGTIGIGAGIGGCAGICGIGGGCCGIGGCIGGTIG 205
                                                                                                          4 GUUUCCGAAAUCGGUGGUGGUGGUGGUGGUGGUGGUGGUCGUCAAACUCCAUGGAACGUGUU 63
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US-10-467-962B-100/C
Sequence 100, Application US/10467962B
Sequence 100, Application US/10467962B
Publication No. US20050246784A1
GENERAL INFORMATION:
APPLICANT: Pleach, Gunnar
APPLICANT: Blau, Astrid
APPLICANT: Daeschner, Klaus
APPLICANT: Klain, Mathieu
TITLE OF INVENTION: Identification of Herbicidally Active Substances
FILE REFERENCE: 2000 857
CURRENT APPLICATION NUMBER: US/10/467,962B
CURRENT FILING DATE: 2003-08-14
CURRENT FILING DATE: 2003-08-14
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin Vers: 2.0
SOFTWARE: Patentin Vers: 2.0
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Query Match 26.9%; Score 25; DB 1; Length 1065; Best Local Similarity 40.0%; Pred. No. 16; Matches 26; Conservative 14; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(2043)
OTHER INFORMATION: ORF K5J14.11, Linie 229091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1704
SOFTWARE: DL SEQ_genes Version 1.0
SEQ ID NO 119
LENGTH: 2218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                             204 GCCTG 200
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US-10-467-962B-100

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APPLICANT: GGGGGAKE, PAUL J.
APPLICANT: GGGGGAKE, PAUL J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sterwood, Steven
APPLICANT: Sterwood, Steven
APPLICANT: Sterwood, Steven
APPLICANT: Tunas, Daniel
APPLICANT: Watenabe, Colin K
APPLICANT: Wood, William
APPLICANT: Abang, Zemin
APPLICANT
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                                                                                                                                                          APPLICANT: AKZO Nobel N.V.
TITLE OF INVENTION: live attenuated parasite vaccine
FILE REPERENCE: 2002-017-EP
CURRENT APPLICATION NUMBER: US/10/526,731
CURRENT FILING DATE: 2002-03-04
FRIOR PAPLICATION NUMBER: EP 02078953
FRIOR PELING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-10-131-826A-531
Sequence 531, Application US/10131826A
Publication No. US20050245730A1
GENERAL INPORMATION:
RESULT 12
US-10-526-731-4
Sequence 4, Application US/10526731
Publication No. US200050244437A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard, Audrey,
Goddowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bareer, Kevin P.
APPLICANT: Bereeini, Murzeen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvavoff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA; ORGANISM: Toxoplasma gondii
US-10-526-731-4
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| Sequence 775, Application US/10821234
| Publication No. US20050255114A1
| GENERAL INFORMATION:
| APPLICANT: Labat. Ivan
| APPLICANT: Stache-Crain, Birgit
| APPLICANT: Andarmani, Susan
| APPLICANT: Andarmani, Susan
| TILE OF INVENITON: Methods for Diagnosis and Treatment of Preeclampsia
| TILE OF INVENITON: Methods for Diagnosis and Treatment of Preeclampsia
| TILE OF INVENITON: WHERE: US/10/821,234
| CURRENT FILING DATE: 2004-04-07
| PRIOR APPLICATION NUMBER: US 60/462,047
| NUMBER OF SEQ ID NOS: 1704
| SOFTWARE: pt -SEQ_genes Version 1.0
| SEQ ID NO 775-
                                                                                                                                                                                                                                                                                                                                              Sequence 255, Application US/10821234

| Publication No. US20050255114A1
| GENERAL INFORMATION:
| APPLICANT: Labat. Ivan
| APPLICANT: Stache-Crain, Birgit
| APPLICANT: Andarmani, Susan
| APPLICANT: Content of Preeclampsia
| TITLE OF INVENTION: WHERE: US/10/821,234
| CURRENT FILING DATE: 2004-04-07
| WIMBER OF SEQ ID NOS: 1704
| SEQ ID NO 255
| LENGTH: 3893
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26.2%; Score 24.4; DB 1; Length 3893;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 16; Conservative 9; Mismatches 1; Indels 0
       DB 1; Length 2043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 26.0%; Score 24.2; DB 1; Length 963; Local Similarity 51.4%; Pred. No. 29; No. 29; No. 29; Conservative 10; Mismatches 8; Indels (
                                                                       1; Indels
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Query Match
26.2%; Score 24.4; Est Local Similarity 69.2%; Pred. No. 29; Matches 18; Conservative 7; Mismatches
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                                                                                                                                       12 AAUCGGUGGUGGUGGUGGUGGUG 37
                                                                                                                                                                            89 AAGCGGTGGTGGTGGTGGTG 64
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US-10-821-234-255
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US-10-821-234-775
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US-10-821-234-775
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; Publication No. US20050253114A1
; GENERAL INFORMATION:
    APPLICANT: Labat, Ivan
    APPLICANT: Stache-Crain, Birgit
    APPLICANT: Argument, Susan
    APPLICANT: Tang, Y. Tom
    TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
    CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
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PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                                                                                      Query Match 25.6%; Score 23.8; DB 1; Length 1 Best Local Similarity 51.2%; Pred. No. 39; Matches 22; Conservative 9; Mismatches 12; Indels
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APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Softer, Simon
APPLICANT: Foster, Simon
APPLICANT: Mond, James
ITILE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: PIOGES9WO
CURRENT PEPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-09-09
NUMBER OF SEQ ID NOS: 424
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/10485517; Publication No. US20050256299A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CRGANISM: Staphylococcus aureus
US-10-485-517-4
                                                                                                                                                                                                                                       , ORGANISM: Homo Sapien
US-10-131-826A-531
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                                                                                                                                                                                                                    TYPE: DNA
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25.6%; Score 23.8; DB 1; Length 14770;
Best Local Similarity 59.3%; Pred. No. 64;
Matches 16; Conservative 9; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                               12126 GGTGGTGGTGGTAGTGGTAGTGGT 12100
                                                                                                                                                                                                                                                                                                                                    16 GGUGGUGGUGGUGGUGGUGGUGGU 42
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 268
LENGTH: 14770
                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-821-234-268
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Human ami

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Norway ra PTH/PTHrP Amino aci Exemplary

Rat PTH ( Parathyro N-Dimethy

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using sw model - protein search, OM protein

November 21, 2005, 16:17:24; Search time 186 Seconds (without alignments) 37.796 Million cell updates/sec Run on:

SEQ-NEW

1 avseiglmhnlggggg 16 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 s

summaries

geneegp2000s:\*
geneegp2001s:\*
geneegp2002s:\*
geneegp2003as:\*
geneegp2003bs:\*
geneegp2003bs:\* geneseqp1980s:\* geneseqp1990s:\* A\_Geneseq\_21:\*
1: genesecr\*
2: rr Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	-	Aay96975 Parathyro	_	Aar58104 [Gly13]-h		~					Adu24382 Novel hum	Adw88336 Rat parat	Adz76832 Parathyro		Adw88343 Rat parat	Aay98016 Human ami	Aay98049 Human par	Aay98045 Human par	Aay98048 Human par	Aay98044 Human par	-	Adq75375 PTH/PTHrP		Aay96978 PTH-rP fu
SUMMARIES	dī	AAY96988	AAY96975	AAY96973	AAR58104	ADZ76826	ABG76365	AAB01861	AAB96896	AAB84776	ADR14864	ADU24382	ADW88336	ADZ76832	ABP71487	ADW88343	AAY98016	AAY98049	AAY98045	AAY98048	AAY98044	AAU73060	ADQ75375	AAY04203	AAY96978
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	* Query Match Length DB	450	31	31	38	12	13	14	14	14	14	14	14	15	21	21	27	27	27	28	28	30	30	31	31
•	& Query Match	85.5	83.1	74.7	74.7	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1
	Score	71	69	62	62	59	59	59	59	29	59	59	59	59	93	59	59	59	59	59	59	59	59	59	29
	esult No.		7	m	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

26         71.1         31         7         ANZ4779         AAZ4779           26         59         71.1         31         3         AAY98015         AAY98015           26         59         71.1         31         3         AAY98015         AAY98015           30         59         71.1         34         2         AAR07927         AAR07920           31         3         AAY98015         AAR07920         AAR07920         AAR07920           32         59         71.1         34         2         AAR07920         AAR07930           31         4         AAR07920         AAR07930         AAR07930         AAR07930           31         4         AAR07900         AAR07900         AAR07900         AAR07900           31         4         AAR07900         AAR07900         AAR07900         AAR07900           31         4         AAR07900         AAR07900         AAR07900         AAR07900           31         4         AAR07000         AAR07900         AAR07900         AAR07900           31         4         AAR07000         AAR07900         AAR07900         AAR07900           31         4         AAR07000 <th>D, 3</th> <th>C 0</th> <th>O G</th> <th>K (</th> <th>z,</th> <th>۹, ۱</th> <th><b>z</b>, (</th> <th>9</th> <th>,</th> <th>٠,</th> <th>1, 11</th> <th>4 12</th> <th>- 4</th> <th>124</th> <th>Œ</th> <th>2.</th> <th>œ</th> <th>Z</th> <th>щ</th> <th><b>4</b></th> <th>щ.</th> <th>x, ı</th> <th></th> <th>4 2</th> <th>-</th> <th>- 12</th> <th>- 2</th> <th></th> <th>, μ</th> <th>. щ</th> <th>1 14</th> <th>-</th> <th>μ,</th> <th>щ</th> <th></th> <th>~</th> <th>•</th> <th>-</th> <th>- '</th> <th>-</th> <th></th> <th>-</th> <th>,</th> <th>-</th> <th>-</th> <th>_</th> <th>-</th> <th></th> <th>-</th> <th></th> <th>-</th> <th>_</th> <th>_</th> <th>_</th> <th></th> <th></th> <th></th> <th></th> <th></th> <th>_</th> <th>_</th> <th>_</th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th>	D, 3	C 0	O G	K (	z,	۹, ۱	<b>z</b> , (	9	,	٠,	1, 11	4 12	- 4	124	Œ	2.	œ	Z	щ	<b>4</b>	щ.	x, ı		4 2	-	- 12	- 2		, μ	. щ	1 14	-	μ,	щ		~	•	-	- '	-		-	,	-	-	_	-		-		-	_	_	_						_	_	_						
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N-alpha-m [Ala1]-hP Rat parat N-alpha-m Rat PTH p Parathyro Rat bioac Mouse bio

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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor enquals sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by
 Aay98046 Human par
Aay98052 Human par
Aab81074 Human par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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/label= PTH-1_receptor
/note= "Human PTH-1 receptor residues 182-593"
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1. .23
/label= Signal sequence
/note= "Human PTH-1 receptor residues 1-23"
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                                                                                                                                                                                                                          Human tethered PTH-1 receptor, Tether-Rll.
                                                                     ALIGNMENTS
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 AAY98046
AAY98052
AAB81074
                                                                                                                                        AAY96988 standard; protein; 450 AA
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/label= PTH(1-11)
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/label= Linker
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7 7 8
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(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
(JUEP/) JUEPPNER H.
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N-PSDB; AAA51737.
67.5
67.5
67.5
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Synthetic.
Chimeric.
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 56 56
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inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
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                                                                                                                                                                                                                                                                                                                             Parathyroid hormone functional domain conjugate peptide PG7
                                                                    Score 71, DB 3; Length 450;
Pred. No. 0.0085;
0; Mismatches 1; Indels
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/label= PTH N-terminal_signaling_domain
/note= "residues 1-9"
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/label= PTH C-terminal_binding_portion
/note= "residues 17-31"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                       AAY96975 standard; peptide; 31 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10. .16
/label= linker
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                                                                      85.5%;
93.3%;
                                                                                                                                    1 AVSEIQLMHNLGGGG 15
                                                                                                                                                    24 AVSEIQLMHNRGGGG 38
                                                                                                                                                                                                                                                                                                   31-OCT-2000 (first entry)
                                                                        Query Match
Best Local Similarity 93.3
Matches 14; Conservative
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N-PSDB; AAA51730.
                                            Sequence 450 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Synthetic.
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Peptide
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and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inn-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrp which avoids the need for regular injections to treat osteoporosis
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                                                                                                                  83.1%; Score 69; DB 3; Length 31; 87.5%; Pred. No. 0.00085;
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//abel= PTH N-terminal_signaling_domain
/note= "resīdues 1-9"
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/label= PTH C-terminal binding portion
/note= "resIdues 15-31"
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                                                                                                                                                                                                                                                                           AAY96973 standard; peptide; 31 AA.
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/label= linker
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                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                14; Conservative
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(POTT/) POTTS J T.
(JUEP/) JUEPPNER H.
                                                                                                                                 Local Similarity
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                                                                                        Sequence 31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                       Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
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                                                                                                                                                 74.7%; Score 62; DB 3; 87.5%; Pred. No. 0.011; ive 0; Mismatches
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92GB-00026815.
92GB-00026851.
92GB-0001691.
93GB-0001692.
93GB-00001693.
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ses 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              [Gly13] -hPTH(1-38) -OH
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Matches 12; Conserv
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                                                                                                                           Sequence 31 AA;
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                                                                                                                                                                                                                                                                                                                                                      20-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1992;
18-DEC-1992;
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23-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                               Matches
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Producing antibodies to a three-dimensional epitope of a bioactive human parathyroid hormone for diagnosing or treating e.g., hyperparathyroidism by immunizing an animal with the hormone and recovering the antibodies.
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Human, three-dimensional epitope; human parathyroid hormone; hPTH; bioactive hPTH; antibody production; hyperparathyroidism; antithyroid; hypoparathyroidism; immunostimulant; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP; calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis; bone synthesis; agonist; osteoporosis; non-parenteral delivery.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [Ala1]-parathyroid hormone peptide(1-14), SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                       (QUES-) QUEST DIAGNOSTICS INVESTMENTS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 10; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB01861 standard; peptide; 14 AA.
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                                                                                                                                                                                                                                                                   03-JUL-2002; 2002WO-US021356.
                                                                                                                                                                                                                                                                                                            03-JUL-2001; 2001US-00898398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AVSEIQLMHNLG 12
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                                                                                                                                                                      WO2003003986-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200023594-A1
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Modified-site
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                           Hutchison JS;
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                                                                                                  Homo sapiens
Synthetic.
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                                                                                                                                                                                                                    16-JAN-2003
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method of producing an antibody to the N-terminal portrion of (1-84) parathyroid hormone (PTH) which comprises administering N-terminal peptide antigens corresponding to amino acid residues 2-12, 1-12, 2-15 and 1-15 of PTH. The methods and compositions of the invention are useful in determining bioactive intact PTH levels in serum, plasma and/or cell culture media and antibodies possessing a high degree of species cross-reactivity. The present esquence is a parathyroid hormone (PTH) (1-12) antigenic N-terminal peptide. This N-terminal peptide sequence is obtained from mouse and rat species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing antibodies to the N-terminal portion of (1-84) parathyroid hormone (PTH) by administering a first peptide antigen to a host animal, useful in determining bioactive intact PTH levels in serum, plasma and/or cell culture media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                    Parathyroid hormone (PTH) (1-12) antigenic peptide, SEQ ID NO: 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 71.1%; Score 59; DB 9; Length 12; Local Similarity 100.0%; Pred. No. 0.012; les 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 5; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                  Parathormone; PTH; hormone; antigen
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                                                                                                                                                                           ADZ76826 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2000; 2000US-00730174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zahradnik RJ, Lavigne JR;
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                                                                                                                                                                                                                                                                     (first entry)
          13
                                      AVSEIQLMHNLG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AVSEIQLMHNLG 12
          AVSEIQLMHNLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZAHR/) ZAHRADNIK R J. (LAVI/) LAVIGNE J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-344980/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2005095236-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
Rattus sp.
                                                                                                                                                                                                                                                                     14-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-2005
                                                                                                                                                                                                                       ADZ76826;
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Matches
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ABG76365
                                                                                                                          REBULT 5
AD276826
AD27682
AD276826
AD27
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hypercalcaemia; anaemia; bone disease; renal impairment; ulcer; myopathy;
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                                                           Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB84776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                     The invention relates to a novel parathyroid hormone (PTH) peptide

(C (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and

(C (AAB01859). The peptides of the invention are at least 85% identical to the

(C (B 01869). The peptides of the invention are at least 85% identical to the

(C (B 01869). The peptide of the invention are at least 85% identical to the

(C (B 01869). The peptide of the formula: X1-Val-Ser-Glu-X2-Gly-Leu-X3-His-X4-X5-

(C (G (A 01869)). The peptide of the formula: X1-Val-Ser-Glu-X2-Gly-Leu-X3-His-X4-X5-

(C (G (A 01869)). The peptide of the formula: X1-Val-Ser-Glu-X2-Gly-Leu-X3-His-X4-X5-

(C (C (C (A 01860))). The peptide of the formula: X1-Val-Ser-Glu-X2-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-Gly-X-
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                                                                                                                                                                        Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                 Jueppner H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB 3;
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                 Sardella TJ, Kronenberg HM, Potts JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB96896 standard; peptide; 14 AA.
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100.0%; Pre
0;
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                 98US-0105530P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                          GARDELLA T J.
KRONENBERG H M.
POTTS J T.
JUEPPNER H.
                                                                                                                                              WPI; 2000-339693/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14 AA;
                 22-OCT-1998;
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                                                                          (POTT/)
                                             (GARD/)
                                                            KRON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osteopathic; calcium homeostasis regulator; parathyroid hormome; PTH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel amino acid encoding polypeptides useful in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
neuropathy; hyperparathyroidism; osteoporosis; fracture cartilage disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potts JT, Juppner H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Native rat parathyroid hormone peptide fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                         Jueppner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.1%; Score 59; DB 100.0%; Pred. No. 0.0 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Potts JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 64; 100pp; English.
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25-FEB-2000; 2000US-0185060P.
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                                                                                                                                                                                                                                                                                                                                                      The present invention relates to parathyroid hormome (PTH) polypeptide derivatives, and the present sequence is one such derivative. PTH is a major regulator of calcium homeostasis. The PTH polypeptide derivatives are useful for treating conditions characterised by decreases in bone mass, such as old age esteoporosis and post-menopausal osteoporosis. The polypeptides are also useful for determining rates of bone reformation, bone resorption and/or bone remodaling, by administering the polypeptide and effective bone mass-increasing amount to the peptide into the bone, by providing to the patient DNA encoding the peptide and expressing the peptide in vivo. The levels of GAMP and inositol phosphate can also be increased in a mammalian cell having PTH-1 receptors, by contacting the cell with a sufficient amount of the polypeptide.
                                                                                                   New Parathyroid hormone (PTH) derivatives useful for treating conditions characterized by decreases in bone mass.
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(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biologically active peptide, parathyroid hormone analogue; endocrine-Gen; antithyroid; cardiovascular-Gen; CNS-Gen; gastrointestinal-Gen; osteopathic; cAMP agonist; bone calcification promoter; parathyroid hormone-1 receptor agonist; calcium antagonist; bone mass; bone reformation; bone resorption; bone resorption; bone recoporasis; osteopenia; bone fracture; cartilage disorder; OTH-1 receptor; human.
The specification describes a method for treating mammalian conditions characterized by a decrease in bone mass. The method comprises administering to a subject a biologically active peptide of a formula given in the specification. The peptide is a parathyroid hormone (PTH) derivative containing amino acid substitutions at selected positions in the polypeptide as well as derivatives containing lactam bridges between receiptor. The method is useful in treating mammalian conditions characterized by a decrease in bone mass e.g. old age or post-menopausal osteoporosis. The present sequence represents a native rat PTH fragment.
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(BRIM ) BRISTOL-MYERS SQUIBB CO.
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Synthetic.
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acting as a cAMP agonist, bone calcification promoter, agonist of parathyroid hormone-1 receptor or calcium antagonist. The invention may be useful for treating mammalian conditions associated with decrease in bone mass or for determining rates of bone reformation, bone resorption and/or bone remodeling. The invention may also be useful for prophylaxis and/or bone reacogling. The invention may also be useful for prophylaxis cxample osteoporosis, osteopenia, fractures and cartilage disorders, and for treating a medical disorder that results from altered or excessive action of the OTH-1 receptor. The present sequence is that of a human parathyroid hormone-derived biologically active peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conformationally constrained parathyroid hormone analogs useful in treatment of e.g. hypercalcemia primary and hyperparathyroidism.
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antithyroid; parathormone; hypercalcemia; metabolic disorder.
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Modified-Bite
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the J domain. The present sequence is that of rat PTH(1-14). PTH derivatives of the invention contain changes in sequence relative to this wide-type sequence. Note: this sequence is given as SEQ ID NO:26 in Figure 1 of the specification, but is different from the sequence given in SEQ ID NO:26 on page 16 ADW88342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing antibodies to the N-terminal portion of (1-84) parathyroid hormone (PTH) by administering a first peptide antigen to a host animal, useful in determining bioactive intact PTH levels in serum, plasma and/or
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100.0%; Pred. No.
:ive 0; Mismatch
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Best Local Similarity 100.
Matches 12; Conservative
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LAVIGNE J R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to conformationally constrained parathyzoid hormone (PTH) analogueues, in particular, derivatives of PTH (1-134), PTH (1-121), PTH (1-124), PTH (1-13), PTH (1-13), PTH (1-114), PTH (1-115), PTH (115), PTH (1-115), PTH (115),                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conformationally constrained parathyroid hormone (PTH) analogs, useful for treating conditions characterized by decrease in bone mass (e.g. osteoporosis) or by the need for bone growth (e.g. in treating fractures or cartilage disorders).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTH; parathyroid hormone; anabolic; cAMP; bone mass; osteopenia; rat.
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                                                                                                                                                                                                                                                                                                                                                                                      Rat parathyroid hormone (PTH) peptide fragment (residues 1-21).
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                                                                                                                                                        ABP71487 standard; peptide; 21 AA.
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02-OCT-2001; 2001US-0326212P.
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The invention provides novel antagonists of the juxtaposition (J) domain of the parathyroid hormone (PTH or parathormone) receptor. These antagonists contain amino acid substitutions at selected positions in truncated PTH and PTH-related polypeptide and function by selectively truncated PTH and PTH-related polypeptide and function by selectively binding the J domain of the receptor. The J domain is the region of the receptor (PIR) that spans the seven transmembrane domain and the extracellular loops. PIR polypeptide antagonists of the invention can be extracellular loops. PIR polypeptide antagonists of the invention can be considered to treat conditions relating to PHPIR hyperactivity, auch as the present and Jansen's chondrodysplasia. They can also be used to identify other ligands (e.g. using a high-throughput screen) that bind to identify other ligands (e.g. using a high-throughput screen) that bind to PIR, such as small molecule PTH mimetic compounds, or for the copies of the invention contain changes in sequence relative to this derivatives of the invention contain changes in sequence relative to this will be the specification, but is significant of the sequence given in SEQ ID NO:27 in Pigure 1 ADW88337.
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Cardiovascular-gen.; CNS-gen.; gastrointestinal-gen.; endocrine-gen.; antithyroid; parathormone; hypercalcemia; metabolic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New conformationally constrained parathyroid hormone analogs useful the treatment of e.g. hypercalcemia primary and hyperparathyroidism.
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99WO-US027863

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24-NOV-1999;
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                                                                                                                                                                                                                                                                      Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the amino terminal is important for signal transduction. The present sequence is a human PTH peptide, with an amino-terminal modification which results in effective activation of the PTH-2 receptor and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteopomia, hypoparathyroidism and hypernalcaenia. In turn, hypercalcaemia is associated with hypernephroma conditions and evariety of cancers: breast, lung and prostate carcinoma, multiple myeloma and epidermoid cancers of the head, neck and oesophagus. This peptide would be suitable for prophylaxis and treatment of the above fracture repair. The present sequence would be suitable for fracture repair. The present sequence is modified to have a desamino constitution.
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                                                                                                                                                                                                      New parathyroid hormone (PTH) analogs having one or more amino acid substitutions that confer PTH-1/PTH-2 receptor agonist properties, useful for treating old age osteoporosis and post-menopausal osteoporosis.
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Pred. No. 0.029;
0; Mismatches 0; Indels
  /note= ."Ala is desamino residue"
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                                                                                                                                                           Gardella TJ;
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Matches 12; Conservative
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                                                                                                               BRINGHURST F R.
                                                                                                                           (TAKA/) TAKASU H.
(GARD/) GARDELLA T J.
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Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the amino terminal is important for signal transduction. Various PTH peptides were produces with amino- and carboxy terminal modifications PTH peptides varying PTH receptor activation properties and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteopaenia, hypoparathyroidism and hypernephroma and a variety of cancers: breast, lung and prostate carcinoma, multiple myeloma and epidermoid cancers of the head, neck and oseophagus. The present sequence is a PTH peptide, with an Ala residue at position 19. The Ala residue improves downstream signalling and ligand binding. PTH peptides with an Arg residue at calcues ptc signalling and ligand binding. PTH peptides with an Arg residue at position 19. The Ala residue improves downstream signalling and ligand binding. PTH peptides with an Arg residue at position pthy are improved PLC signalling and ligand binding. PTH peptides with an Arg residue at position supposed PLC signalling and ligand binding pthy for the treatment of the above mentioned disorders and fracture repair
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                                                                                                                                                                                                                                                                                   Novel biologically active peptide comprising a parathyroid hormone peptide derivative, useful for treating osteoporosis.
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                                                                                                                                         Potts JT;
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0; Mismatches
                                                                                                                                         Gardella TJ,
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98US-0109938P
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25-NOV-1998;
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Page 10

Gardella TJ, Potts JT;

Takasu H,

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calls, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the amino terminal of PTH is important for PTH receptor binding, while the amino terminal is important for gignal transduction. Various PTH peptides were produces with amino- and carboxy terminal modifications which had varying PTH receptor activation properties and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteopaenia, hypoparathyroidism and mucher of disorders. In turn, hypercalcaemia is associated with hypernephroma and avariety of cancers: Dreast, lung and prostate carcinoma, multiple myelome and epidermoid cancers of the head, neck and oesophagus. The present sequence is a PTH peptide, with an Ala residue at position 19. The Ala and Arg residues both improve downstream signalling via phospholipase C (PLC) and ligand binding. The treatment of the above mentioned disorders. In addition, the present repetions would be suitable for fracture repair
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                                                                   Novel biologically active peptide comprising a parathyroid hormone peptide derivative, useful for treating osteoporosis.
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                                                                                                                        Disclosure; Page 68; 75pp; English.
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Best Local Similarity 100.
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                                    WPI; 2000-400076/34.
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cells, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the carboxyl terminal of PTH is important for PTH receptor binding, while the anino terminal is important for signal transduction. Various PTH peptides over produces with anino- and carboxy terminal modifications which had varying PTH receptor activation properties and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteopor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel biologically active peptide comprising a parathyroid hormone peptide derivative, useful for treating osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY98044 standard; peptide; 28 AA.
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Claim 8; Page 69; 75pp; English.
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Les 12; Conservative
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Gaps

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71.1%; Score 59; DB 3; Length 27; 100.0%; Pred. No. 0.029; ive 0; Mismatches 0; Indels

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were produces with amino- and carboxy terminal modifications which had varying PTH receptor activation properties and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteoperosis, osteopenia, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma and a variety of cancers: breast, lung and prostate carcinoma, multiple present sequence is a PTH peptide, with an Ala residue at position 1 and an Arg residue at position 19. The Ala and Arg residues both improve downstream signalling via phospholipase C (PLC) and ligand binding. The present peptide may therefore be used as a PTH receptor agonist for the treatment of the above mentioned disorders. In addition, the present sequence would be suitable for fracture repair
                  88888888888888888888888888
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Sequence 28 AA;

ö Query Match
Pest Local Similarity 100.0%; Pred. No. 0.03;
Matches 12; Conservative 0; Mismatches 0; Indels

1 AVSEIQLMHNLG 12

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Search completed: November 21, 2005, 16:38:10 Job time : 189 secs

Colosus Middle Scot S.

seq-new.rpr

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                                                                                          November 21, 2005, 16:30:49; Search time 38 Seconds (without alignments) 40.512 Million cell updates/sec
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              5.1.6
Compugen Ltd.
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1: pir1: *
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Perfect score:
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## ALIGNMENTS

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A; Reference number: $21199; MUID:92209518; PMID:1555591
A; Reference number: $21199; MUID:92209518; PMID:1555591
A; Recession: $21199; MUID:92209518; PMID:1555591
A; Modecule type: protein
A; Residues: $3-214, W; CLS.
A; Cross references: WIPARC:UD10000173485
A; Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation;
A; Natl, H.D.; Sauer; R.T.; Jacobe, J.W.; Reuthann, H.T.; Segre, G.V.; O'Riordan, J.L.H.;
RN: Natl, Accession: A3379; MUID:74111656; PMID:4521809
A; Recession: A33799; MUID:74111656; PMID:4521809
A; Residues: 32-68 - MID:A; PMID:451809
A; Residues: 32-68 - MID:A; PMID:451809
A; Residues: 32-68 - MID:A; A. 69; 3365-3588
B; Rever Jr.; H.B.; Paixwell T.; Ronnan, R.; Sizemore, G.W.; Arnaud, C.D.
B; Reference: UNIPARC:UD10000120405
A; Residues: 32-52, O', 54-58, K', 60, 'L', 62-65 CRE>
A; Recence number: A33783
A; Molecule type: protein
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A; Molecule type: protein
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A; Recence number: A33873
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A; Residues: 32-52, O', 54-58, K', 60, 'L', 62-65 CRE>
A; Recence number: A33873
A; Molecule type: protein
A; Residues: 52-75 CRE3>
A; Recence number: A33873
A; Recence number: A3387
A; Recence number: A3485
A; Reference number: A348
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 24.Apr-1994 #sequence revision 19-Jan-1996 #text change 09-Jul-2004
C; Date: 24.Apr-1994 #sequence 22109; A93789; A93789; A90387; A90426; A94410; I387
C; Accession: A19339; S53790; A93169; S21199; A93789; A93789; A90387; A90426; A94410; I387
R; Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J
Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
A; Rftle: Nucleotide sequence of the human parathyroid hormone gene.
A; Recence number: A19339; MUID:83169834; PMID:6220408
A; Recence number: A19339; MUID:83169834; PMID:6220408
A; Residues: U.II5 < VAA>
A; Recence number: A33790; MUID:95225988; PMID:7710697
A; Residues: VX. 33.AX, 35-46;65-84;105-110 < VAM>
A; Residues: VX. 33.AX, A; A; Remper: A33169; MUID:74174967; PMID:4833516
A; Roccession: A33169

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A;Residues: 61-106, D'. 108-115 <KEU>
A;Cross-references: UNIPARC:UP100001734E8
A;Cross-references: UNIPARC:UP100001734E8
R;Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.!
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-1
                                                                                                                                                                                                                                                            Cybecies: Rattus norvegicus (Norway rat)
Cybecies: Rattus norvegicus (Norway rat)
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Cybecies: Rattus norvegicus (Norway rat)
Cybecies: Rattus norvegicus (Norway rat)
Cybecies: A05091; A26806
RyHeinrich, G.; Kronenberg, H.M.; Potts Jr., Jr.; Habener, J.F.
J. Biol. Chem. 259, 3320-3329, 1984
A;Reference number: A05091; MUID:84135846; PMID:6321505
A;Rocesion: A05091
A;Rocesion: A05091
A;Rocesion: A05091
A;Roces: H.J.; Gross, G.; Midera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3528009
A;Rocesion: A26806
A;Rocesion: A26806
A;Rocesion: A26806
A;Rocesion: A26806
A;Rocesion: A26806
A;Rocesion: A26806
A;Cross-references: UNIPARC:UPI000013290C; GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA291
C;Genetics: 29/3
A;Introns: 29/3
A;Introns: 29/3
A;Introns: 29/3
A;Introns: Parathyroid hormone; parathyroid hormone homology PTH>
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151851
parathyroid hormone - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: 151851
R;Schmelzer, H.
Adv. Gene Technol. 21, 228-229, 1984
A;Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A;Reference number: 151851
A;Atatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-105 <RES>
A;Cross-references: UNIPARC:UP10000170AE0; GB:MS4875; NID:g601932; PIDN:AAA57156.1; PID: C;Genetics:
A;Genetics:
A;Genetics:
A;Gene: PTH
C;Superfemnily: parathyroid hormone; parathyroid hormone homology
F;20-54/Domain: parathyroid hormone homology <PTH>
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Pred. No. 0.029;
1; Mismatches 0; Indels
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71.1%; Score 59; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 12; Conservative 0; Mismatches 0; Indels
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1 AVSEIQLMHNLG 12 AVSEIQLMHNLG 43

à g RESULT 3
PIHU
parelyroid hormone precursor (validated)
N/Alternate names: proparathyroid hormone

22 AISEIQLMHNLG 33

1 AVSEIQLMHNLG 12

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Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative

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A; Molecule type: protein
A; Residues: 32-109 < SAU>
A; Crossures: 32-109 < SAU>
A; Crossures: 32-109 < SAU>
A; Crossures: 32-109 < SAU>
A; Crossured: 12-109 < SAU>
A; Crossured: 12-109 < SAU>
A; Crossured: 15, 759-766, 1974
A; Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormonth
A; Reference number: A90030; MUID:74173303; PMID:4598526
A; Contents: annotation
C; Superfamily: parathyroid hormone; parathyroid downone homology
C; Superfamily: parathyroid hormone; parathyroid gland
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 25-31/Domain: popoptide #status experimental <PRO>
F; 30-64/Domain: parathyroid hormone homology <PHT>
F; 30-64/Domain: parathyroid hormone homology <PHT>
F; 32-115/Product: parathyroid hormone #status experimental <PND>
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C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534
E;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.
A;Title: 1801ation and complete nucleotide sequence of the gene for bovine parathyroid has A;Reference number: A24949; MUID:84262483; PMID:6086460
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A;Cesideer 1-115 <WEA>
A;Crossleer 1-115 <WEA
A;C
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A;Title: The amino acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162; PMID:5531031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-115 <KRO>
A; Residues: UNIPARC: UP10000132907; GB:V00106; GB:J00023; NID:g84; PIDN: CAA23439.
A; Cross-references: UNIPARC: UP10000132907; GB:V00106; GB:J00023; NID:g84; PIDN: CAA23439.
A; Note: the authors translated the codon GAA for residue 50 as Gly
R; Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.V.:
Proc. Natl. Acad. Sci. U. S.A. 71, 633-656, 1974
A; Title: The N-terminal amino-acid sequence of bovine proparathyroid hormone.
A; Reference number: A93793; MUID:74142666; PMID:4522780
                                                                                                                               R;Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., Biochemistry 13, 1994-1999, 1974
A;Title: The amino acid sequence of porcine parathyroid hormone.
A;Reference number: A90376; MUID:7425317; PMID:4840833
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Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970
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A;Residues: 26-115 <HAM>
A;Cross-references: UNIPARC:UP100001734DF
                                                                                                   A;Cross-references: UNIPARC:UP100001592DF
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ilarity 91.7%;
Conservative
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Les 11; Conserv
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: B26806; A90390; A90390; A01535
R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Tatle: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid horm
A;Reference number: A26806; MUID:87316938; PMID:3628009
A;Accession: B26806
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-115 <CGH;
A;Cross-references: UNIPROT:P01269; UNIPARC:UPI000013290B; GB:X05722; GB:Y00409; NID:918
R;Chu, L.L.H.; Huang, W.Y.; Littledike, B.T.; Hamilton, J.W.; Cohn, D.V.
Biochemistry 14, 3631-3635, 1975
A;Title: Porcine proparathyroid hormone. Identification, biosynthesis, and partial aminc
                                                                                                                                                                                            A; KEUGUBE: 7-100 KARD.

A; KTEGEAT G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parbons, J. RTEGEAT, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parbons, J. R; Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parbons, J. A; Title: SeyJer's Z. Physiol. Chem. 355, 415-421, 1974

A; Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of hum A; Reference number: A91660; MUID:75059220; PMID:4474131

A; Contents: annotation; synthesis of residues 32-65

A; Note: the biologically active amino-terminal 34 residues of parathyroid hormone were sat renal adenylate cyclase assay and with the bovine hormone's active region in the chic R; Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel, Helv. Chim. Acta 56, 470-473, 1973

A; Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.

A; Reference number: A91635; MUID:73227467; PMID:4721748

A; Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level R; Hendy, G.N.; Kronenberg, H.M.; Potter, J. J. J. J. Proc.

Proc. A; Reference number: 138342; MUID:82150870; PMID:6950381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPARC: UP1000013290A; EMBL: V00597; NID: 937143; PIDN: CAA23843.1; PID
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A;Cross-references: GDB:119522; OMIM:168450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: 138342
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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A;Reference number: A94410
A;Accession: A94410
A;Molecule type: protein
A;Residues: 75-100 <KE2>
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parathyroid hormone precursor - dog
parathyroid hormone precursor - dog
Cispecies: Canis lugus familiaris (dog)
Cjacces: Canis lugus familiaris (dog)
Cjaccession: 04202
Rycession: 04202
Cjaccession: 04203
Cjaccession: 0420
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A,Status: prelimary; translated from GB/EMBL/DDBJ
A,Status: prelimary; translated from GB/EMBL/DDBJ
A,AStatus: prelimary;
A,Residues: 1-119 «KHO»
A,Residues: 1-119 «KHO»
A,Residues: 1-119 «KHO»
A,Cross-references: UNIPARC:UPIO000132909; GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g
C,Superfamily: parathyroid hormone; parathyroid hormone homology
F;1-25/Domain: signal sequence #status predicted «SIG»
F;2-3-10-ADomain: propeptide #status predicted «PTH»
F;30-34/Domain: parathyroid hormone homology «PTH»
F;30-64/Domain: parathyroid hormone #status predicted «MAT»
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Pred. No. 6.9;
3; Mismatches 3; Indels
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63.9%; Score 53; DB 2; Length 119;
Best Local Similarity 83.3%; Pred. No. 0.21;
Matches 10; Conservative 2; Mismatches 0; Indels
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Best Local Similarity 57.1%;
Matches B; Conservative
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32 SVSEIQFMHNLG 43
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A,Gene: MTH793
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Aritle: Bovine parathyroid hormone: amino acid sequence.

Arcession: A93773; MUID:71063634; PMID:5275384

Arcession: A93773; MUID:71063634; PMID:5275384

Arcession: A93773; MUID:71063634; PMID:5275384

Arcession: A93773; MUID:710600043284

Arcession: A1.7.7 Tregear, G. W.; Koutmann, H.T.; Miall, H.D.; Sauer, R.; Deftos, L.J.;

Broot. Mail. Acad. Sci. U.S.A. 68, 61-67, 1937

Aritle: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyr

Aritle: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyr

Aritle: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyr

Aritle: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyr

Aritle: Algorithms: amotation: synthesis of residues 32-68

Aritle: Med. Sci. 193746; MUID:71091889; PMID:4322656

Aritle: Recent studies on the chemistry of human, bovine and porcine parathyroid hormon

Areference number: A30030; MUID:74173303; PMID:4598526

Aritle: Anterdoction by molecular clouding of artifactual inverted sequences at the S' the Arcessides: 115 eMED.

Arcessides: Aritle: Muid: Aritle: A
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A34917

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F;26-115/Product: proparathyroid hormone #status experimental <PNAT>
F;26-31/Domain: propeptide #status experimental <PRO>
F;30-44/Domain: parathyroid hormone homology <PH>
F;32-115/Product: parathyroid hormone #status experimental <MAT>
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Best Loc Matches

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A,Cross-references: "NUTROT: P05219; UNIDARC: UDI0000136A39; EMBL: AL031743; PIDN: CAA21099.]
A,Experimental source: strain 972h-; cosmid c26H8
R,Radcliffe, P.; Hirata, D.; Childs, D.; Vardy, L.; Toda, T.
R,Radcliffe, P.; Hirata, D.; Childs, D.; Vardy, L.; Toda, T.
A,Title: Identification of novel temperature-sensitive lethal alleles in essential beta-fa,Reference number: Z22579; MUID:98324923; PMID:9658169
A,Accession: T43623
A,Accession: T43623
A,Accession: T4862
A,Robecule type: DNA
A,Residues: 1-448 «RAD>
A,Residues: 1-448 «RAD>
A,Residues: UNIDARC: UDI0000136A39; EMBL: AF042827; PIDN: AAC21454.1
A,Experimental source: strain 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross_references: UNIPROT:066668; UNIPARC:UPI00000F0F2B; GB:U20824; NID:g695172; PIDN::
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
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A;Cross-references: UNIPARC:UPI000007A51C; EMBL:U29441; NID:gl322213; PIDN:AAC47210.1; Å
A;Experimental source: ATCC 50330
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C;Species: Hexamita sp.
A;Variety: ATCC 50330
C;Date: 21-Apr-1997 #sequence_revision 21-Apr-1997 #text_change 07-Dec-1999
C;Accession: 570637
F;Keeling, P.J; Doolittle, W.F.
EMBO J. 15, 2285-2290, 1996
A;Title: A non-canonical genetic code in an early diverging eukaryotic lineage.
A;Reference number: 870634; MUID:96208514; PMID:8641293
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C.Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
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R;Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
d, Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
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preliminary; translated from GB/EMBL/DDBJ
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A; Status: nucleic acid sequence not shown
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A; Introns: 4/3; 21/2; 35/2; 53/3; 349/1
C; Superfamily: tubulin
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Best Local Similarity 63.0.
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A;Residues: 1-456 <T
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C; Species: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C; Accession: A21649
R; Hiraoka, Y; Toda, T; Yanagida, M.
Cell 39, 349-358, 1984
A; Title: The NDA3 gene of fission yeast encodes beta-tubulin: a cold-sensitive nda3 muta
A; Reference number: A21649; MUID:85048945; PMID:6094012
A; Accession: A21649
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-448 <-HIR-
A; C; Superfamily: tubulin
                                                                                                                                                                                                                            beta tubulin, temperature sensitive - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43624
R;Radcliffe, P.; Hirata, D.; Childs, D.; Vardy, L.; Toda, T.
Mol. Biol. Cell 9, 1757-1771, 1998
A;Title: Identification of novel temperature-sensitive lethal alleles in essential beta-A;Title: Identification of novel temperature-sensitive lethal alleles in essential beta-A;Accession: T43624
A;Accession: T43624
A;Accession: T43624
A;Accession: UNIDENT: DOS219; UNIPARC: UPI0000168807; EMBL: AF042828; PIDN: AAC21455.
A;Experimental source: strain 972
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beta tubulin - fission yeast (Schizosaccharomyces pombe)

beta tubulin - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Species: 33-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T40019; T43623

C;Accession: T40019; T43623

R;Wood, V; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.

A;Reference to the EMBL Data Library, September 1998
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A;Introns: 4/3; 21/2; 35/2; 53/3; 349/1
C;Superfamily: tubulin
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361 AEIGMTHNIGGTGG 374
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probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: A84497
R;Lin, X.; Kaul, S; Roonin; L.A.; Shen, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; h
M; Koo, H; Moffat, K.S.; Cronin; L.A.; Shen, M.I.; Town, C.D.; Fujii, C.Y.; h
Mature 402, 761-768, 1999
A;Rute 402, 761-768, 1999
A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Accession: A84497
A;Accession: A84497
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-962 <STO>
A;Cross-references: UNIPROT:092QM1; UNIPARC:UPI0000AB92C; GB:AE002093; NID:g4263654; PII
A;Gene: At2g1130
A;Map position: 2
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By 4638

By 684638

C. Species: Arabidopsis thaliana (mouse-ear cress)

R. Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; h

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Altile: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A; Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White, K.

Submitted to the EMBL Data Library, September 1993

A; Reference number: 837177

A; Accession: 837177

A; Status: prelimnary

A; Molecule type: mRNA

A; Mesiduae: 1.450 cMIT>

A; Cross-references: UNIPROT: P41385; UNIPARC: UPI0000136A12; EMBL: X74951; NID: g402173; PIDR C; Superfamily: tubulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tubulin beta chain - silkworm
C;Species Bombyx mori (silkworm)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 837177
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54.2%; Score 45; DB 2; Length 962;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 3; Indels
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656 VQLTHRLGGRGG 667
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134 QLVHSLGGGTG 144
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134 QLIHSLGGGTG 144
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Experimental source: Clone F55C5
R;Harris, B
A;Experimental source: Clone F55C5
R;Harris, B
S;Marris, B
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A27421
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A27421
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A27424
A2
A,Note: the sequence of residues 388-395 and the corresponding nucleic acid sequence are C,Genetics:
A,Genetic code: SGC5
C,Superfamily: tubulin
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122.16
hypothetical protein T04H1.9 - Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T22.718; T24481
Sylarris, B.
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Pred. No. 17;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                        2; Length 395;
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Pred. No. 15;
2; Mismatches
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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134 QLIHSLGGGTG 144
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241 LHGLGGGGG 249
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Job time : 40 secs
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R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.B.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A; Authors: Perreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajian, J.P.; Krieger, J.E.; Kuranne, E.E.; Laigit chado, M.A.; Madeira, A.M.B.N.; Matsikuma, J.P.; Krieger, J.E.; Warques, M.V.; Martins, E.G.; Nunes; Martins, E.M.; Matsikuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; de Salva, R.C.; Palmieri, D.A.; Authors: da Silva, A.C.R.; da Silva, R.R.; da Silva, M.A.; Sawasak A.; Eruhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A.; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein P2009.190 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress)
C;Species: Arabidopsis thaliana (Mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession T04621
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, October 1998
A;Reference number: Z15380
A;Accession: T04621
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copper homeostasis protein XP1341 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18 Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession B82694
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                    PI
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A; Molecule type: DNA
A; Residues: 1-267 <SINA
A; Cross-references: UNIPROT: O9PDN8; UNIPARC:UP100000C26D0; GB:AE003966; GB:AE003849; NIC
A;Accession: E84638
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196 <STO>
A;Cross-references: UNIPROT:Q9SJA6; UNIPARC:UPI000000C588; GB:AE002093; NID:g4572679;
C;Genetics:
A;Gene At2g24590
A;Map position: 2
C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
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                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2; Length 196;
Pred. No. 10;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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49 VELCHGLGGGG
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Gaps
A.Cross-references: UNIPROT:049459; UNIPARC:UPI00000A2285; EMBL:AL021749
A.Experimental source: cultivar Columbia; BAC clone F2009
C.Genetics:
A.Map position: 4
A.Introns: 50/3; 114/1
A.Note: F2009.190
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                                                                                                                                                                      53.0%; Score 44; DB 2; Length 305; 77.8%; Pred. No. 16; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                    Best Local Similarity 77.8
Matches 7; Conservative
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completed: November 21, 2005, 16:38:53

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                                                                                                    November 21, 2005, 16:31:04 ; Search time 234 Seconds (without alignments) 48.241 Million cell updates/sec
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ALIGNMENTS

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PHTY RAT

PTHY RAT

AC P04089; O63473;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-NOV-1986 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
DE Ratus norvegicus (Rat).
OS Ratus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchoncoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Sciurognathi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
NGBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                             Gaps
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STRAIN=Speciague Dawley;

RA MUCLEOTIDE SEQUENCE.

RA MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;

RA MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;

RA SEQUENCE analysis of hypothalamic parathyroid hormone messenger are inconveleic acid ";

Endocrinology 136:5600-5607(1995).

REMBL; S80127; AAP32220.1; -; mRNA.

CO; GO:0005576; C:extracellular region; IEA.

RO; GO:0005576; C:extracellular region; IEA.

RO; GO:0005576; Pibrormone activity; IEA.

InterPro; IPR001415; Parathyrd.hrm.

InterPro; IPR001415; Phyrhorm—sub.

PRANTHER; PFRR10541; Phyrhorm—sub.

PRANTHER; PFRR10541; Phyrhorm—sub.

PRANTHER; PRO105429; Parathyroid; 1.

PROSONE; PRONOS3; PTH; 1.

PROSONE; PRONOS3; PRANTHYROID; 1.
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WICLEOTIDE SEQUENCE.
MEDLINE=84135846; PubMed=6321505;
Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 71.1%; Score 59; DB 2; Length 105; Local Similarity 100.0%; Pred. No. 0.2; es 12; Conservative 0; Mismatches 0; Indels
          Query Match 71.1%; Score 59; DB 2; Length 31; Best Local Similarity 100.0%; Pred. No. 0.051; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       080W22;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothalamic parathyroid hormone.
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980WZZ RAT

D Q80WZZ RAT

D Q80WZZ RAT

D 01-UJNN-2003 (TrEMBLrel. 24, DT 01-UJNN-2003 (TrEMBLrel. 24, DT 01-UJN-2003 (TrEMBLrel. 24, DT 01-UJN-2003 (TrEMBLrel. 24, DT 01-UN-2003 (TrEMBLrel. 24, DT 01-UN-2003 (TrEMBLrel. 24, DE Hypothalamic parathyroid has Ratus norvegicus (Rat).

OC Bukaryota; Metazoa; Chordai OC Muridae; Murinae; Rutus OC Muridae; Murinae; Ratus.

OX NCBI_TaxID=1016;

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RP NUCLEOTIDE SEQUENCE.

RA NULLEOTIDE SEQUENCE.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mamalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Sigmodontinae, Peromyscus.
                                                                                                                                                                                                                                                                                                                                                                                                                         Peromyscus maniculatus (Deer mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Sigmodontinae; Peromyscus.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF382593, AAK63072.1; -; Genomic_DNA.
HSSP; P01270; 1ZWB.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005576; F:hormone activity; IEA.
InterPro: IPR001415; Parathyrdom_sub.
PANTHER; PTHRA.0541; Pthyrhorm_sub.
PROSTE; PS00335; PARATHYROID; 1.
ProDom; PD0106687; Pthyrhorm sub.;
ProDom; PD010687; Pthyrhorm sub.;
ProDom; PD010687; Pthyrhorm sub.;
ProDom; PN01279; Parathyroid; 1.
ProDom; PN01279; ARATHYROID; 1.
FN0N_TER 31 A3461 MW; A208B0E772B9B55B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.1%; Score 59; DB 2; Length 31; 100.0%; Pred. No. 0.051; tive 0; Mismatches 0; Indels
RESULT 1

Q11Y90_PERMA

TO Q11Y90.

AC Q91Y90.

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DT 01-UUN-2003 (TrEMBLrel. 24, Last annotation update)

DT 01-UUN-2003 (TrEMBLrel. 24, Last annotation update)

DT 01-UUN-2003 (TrEMBLrel. 24, Last annotation update)

DN Name=Pthy.

SPECTOMYSEUS MEDICALS (Decreased)

OC MURIATOR EURHERIA (Deer mouse).

OC MURIATOR EURHERIA (Deer mouse).

OC MURIAGe: SignonGontinae, Peromyscus.

OC MURIAGe: SignonGontinae, Peromyscus.

ON NCBI TAXID=10042;

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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Parathyroid hormone (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 AA.
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O191791 PERPL

ID 051791 PERPL

AC 091791,
DT 01-DEC-2001 (TrEMBLrel. 19,
DT 01-DEC-2001 (TrEMBLrel. 19,
DT 01-DEC-2001 (TrEMBLrel. 19,
DT 01-UN-2003 (TrEMBLrel. 19,
DE PARATHYCOIG (TREMBLREL. 19,
DE PARATHYCOIG (TREMBLREL. 19,
DE RAINTAGE, SIGMOGONIC (Prodata)
OC Muntade, Sigmodontine, Perc
OX MCBL TaxID=42413,
RN [1]

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les 12; Conservative
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                                                                                                                                                                                                                                                           TISSUE=Parathyroid;
Schmelzer H.J., Gross G., Mayer H.;
"Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinology 136:5600-5607 (1995).
-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
"Gene encoding parathyroid hormone. Nucleotide sequence of the rat
gene and deduced amino acid sequence of rat preproparathyroid
                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 32-115.
STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
MEDLINE=96079910; PubMed=7588314; DOI=10.1210/en.136.12.5600;
NULLEY M.T., Parimi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Hypothalamus and parathyroid gland.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59; DB 1; Length 115;
                                                                                                                                    Schmelzer H.-J., Gross G., Widera G., Mayer H.; "Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat."; Nucleic Acids Res. 15:6740-6740(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C -> Y (in Ref. 3).
A -> T (in Ref. 3).
V -> I (in Ref. 3).
V -> G (in Ref. 3).
W; 7B434CPCA528B230 CRC64;
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Ensembl; ENSRNOG0000014318; Rattus norvegicus.
RGD; 3440; Pth.
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EMBL; XO5721; CAA29192.1; -; mRNA.
EMBL; M54875; AAA57156.1; -; mRNA.
EMBL; SO127; -; NOT_ANNOTATED_CDS; mRNA.
PIR; A05091; A05091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; IPR001415; Parathyrd hrm.
InterPro; IPR003626; PTH related.
InterPro; IPR003625; PTH related.
InterPro; IPR003625; PTH related.
INTERPO; PR003625; PTH; I.
ProDom; PR01272; Parathyroid; 1.
ProDom; P001083; PTH; I.
ProDom; P0010887; PTH; I.
PROSITE; P8000387; PTH; I.
PROSITE; P800035; PTH; I.
PROSITE; P800335; PTH; I.
PROSITE; P800335; PTH; I.
PROSITE; P800335; PTH; I.
PROSITE; P800335; PTH; I.
                                                                                                                                                                                                                                                                                                                                       Adv. Gene Technol. 21:228-229(1984).
                                                            Biol. Chem. 259:3320-3329(1984)
                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE=87316938; PubMed=3628009;
                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF 10-115.
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Marches 12; Conservative
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MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

M. Klausber R. D., Felingold E. A., Grouse L. H., Derge J. G.,

K. Klausper R. D., Collins F. S., Wagner L. Schemen C. M., Schuler G. D.,

Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,

A physins R. F., Jordan H., Moore T., Wax S. I., Wang J., Heiseh F.,

Diatchenko L., Marusina K., Parmer A. A., Rubin G. M., Hong L.,

Staplecon M., Soares M. B., Bonaldo M. F., Casavant T. L., Scheetz T. E.,

Brownstein M. J., Usdin T. B., Toshhyuki S., Carninci P., Prange C.,

Raha S. A., McEwan P. J., McKerran K. J., Abramson R. D., Mullahy S. J.,

Richards S., Worley K. C., Hale S., Garcia A. M., Gubbs R. A.,

Villalon D. K., Muxny D. M., Sodergren E. J., Lu X., Gibbs R. A.,

Kachards S., Worley K. C., Hale S., Garcia A. M., Gabbs R. A.,

Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,

Mhiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,

Radriguez A. C., Grimwood J., Schmutz J., Myers R. M.,

Rodriguez A. C., Grimwood J., Schmutz J., Marra M. A.,

Schmerch A. Schehin J. E., Jones S., M., Marra M. A.,

Schmerch A. Schehin J. E., Jones S., M., Marra M. A.,

Schmerch A. Schehin J. E., Jones S., M., Marra M. A.,

Schmerch A. Schehin J. E., Jones S., M., Marra M. A.,

Schmerch A. Schehin J. E., Jones S., M., Marra M. A.,
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                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinee; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M., "Cloning of the murine gene encoding parathyroid hormone: genomic organization and nucleotide sequence."; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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EMBL, AF066075; AAC99656.1; -; Genomic_DNA.
EMBL, BC099456; AAH99456.1; -; mRNA.
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DA43FABBCB4E2FD9 CRC64;
                                                                                    01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Ensembl; ENSMUSG0000059077; Mus musculus.
MG1; MG1:97799; Pth.
GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005615; P:hormone activity; IDA.
GO; GO:0005074; P:calcium ion homecetasis; TAS.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR00155; Pthyrhorm_sub.
PANTHER; PTHRA0541; Pthyrhorm_sub;
Pfam; PP01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
            115 AA
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SMART; SM00087; PTH; 1.
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                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, La Parathyroid hormone precursor.
Q9Z0L6_MOUSE PRELIMINARY;
Q9Z0L6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sednences.
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115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Thyroid;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhin; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                Gaps
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Shiue Y.-L., Caetano A.R., Lyons L.A., O'Brien S.J., Laughlin T.F., Murray J.D., Bowling A.T., Submitted (MAR.1999) to the EWBL/GenBank/DDBJ databases.

EWBL; AF134233, AAF62347.1; -; Genomic_DNA.

HSSP, POLT20; ETI.

GO; GO:0005170; ETI.

InterPro; IPR001415; Parathyrd hrm.

InterPro; IPR001415; Parathyrd hrm.

InterPro; IPR001425; Parathyrd meub.

Pfam; PF01279; PRTR10441; Phyrhorm gub; 1.

Pfam; PF01279; Parathyroid; 1.

Pfam; PF01279; Parathyroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1)

WUCLECTIDE SEQUENCE.

WEDLINE=20082971; PubMed=10613847; DOI=10.1101/gr.9.12.1239;

Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,

Bowling A.T., Murray J.D.;

"A comparative gene map of the horse (Equus caballus).";

Genome Res. 9:1239-1249(1999).
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13-AUG-1987 (Rel. 05, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).
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Query Match 71.1%; Score 59; DB 2; Length 115; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 12; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.48;
1; Mismatches 0; Indels
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01-OCT-2000 (TrEWBLrel. 15, Last sequence update)
01-JUM-2003 (TrEWBLrel. 24, Last annotation update)
Parathyroid hormone (Fragment).
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Local Similarity 91.7%;
Les 11; Conservative
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Q9N1VO;
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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DT 113-AUG-
DT 13-AUG-
DT 13-AUG-
DT 13-AUG-
DT 10-AUG-
DT 11-AUG-
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REDILERS-8126800, Pubmeds 5950311, W. Petts J.T., Rich A., Mucleocide sequence of clored cubwa encoding human preproparathyroid RT Mucleocide sequence of clored cubwa encoding human preproparathyroid RT Demons. REDILERS-818681, Pubmeds-820408, Mucleocide sequence of clored cubwa encoding human preproparathyroid REDILERS-818681, Pubmeds-820408, Mucleocide sequence of clored cubwa encoding human preproparathyroid sequence of clored cubwa encoding human preproparathyroid sequence of clored cubwa encoding encoding sequence of clored cubwa encoding encoding processes and clored cubwa encoding processes encoding enco
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Sunthornthepvarakul T., Churesigaew S., Ngowngarmratana S.;
"A novel mutation of the signal peptide of the preproparathyroid
hormone gene associated with autosomal recessive familial isolated
hypoparathyroidism.";
J. Clin. Endocrinol. Metab. 84:3792-3796(1999).
-! FUNCTION. PTH elevates calcium level by dissolving the salts in
bone and preventing their renal excretion.
-! SUBCELIULAR LOCATION: Secreted.
-! DISEASE: Defects in PTH are a cause of familial isolated
hypoparathyroidism (FIH) (MIN:146200]. FIH exist both as autosomal
dominant and recessive forms of hypoparathyroidism.
-! SIMILARITY: Belongs to the parathyroid hormone family.
Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H., "Investigation of the solution structure of the human parathyroid hormone fragment (1-34) by 1H NNR spectroscopy, distance geometry, and molecular dynamics calculations.";
                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 32-70.
MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;
Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
"Solution structures of human parathyroid hormone fragments hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";
Biochem. Biophys. Res. Commun. 267:213-220(2000).
                                                                                                                                                                                                       STRUCTURE BY NMR OF 32-68.
MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;
Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.
                                                                                                            MEDLINE-93345518; PubMed-8334299;
Barden J.A., Cuthbertson R.M.;
"Stabilized NMR structure of human parathyroid hormone(1-34).";
Eur. J. Blochem. 215:315-321(1993).
                                                                                                                                                                                                                                                                                        "Structure of human parathyroid hormone 1-37 in solution."; J. Biol. Chem. 270:15194-15202(1995).
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Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.
Kronenberg H.M.;
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EMBL; V00597; CAA23843.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypoparathyroidism.";
J. Clin. Invest. 86:1084-1087(1990)
                                                                     Biochemistry 30:6936-6942(1991)
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Model; A=32-65.
                                                                                                     STRUCTURE BY NMR OF 32-65.
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NWR; @=32-68.
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NWR; @=32-65.
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NWR; @=33-68.
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@=35-68.
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PubMed=10523031;
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Mary, 402.00; G. (Cextracellular region; NAS.)

RGO; GO; 0005579; E: hormone activity; TAS.

RGO; GO; 0006579; E: hormone activity; TAS.

RGO; GO; 0006674; P: calcium ion homeostasis; NAS.

RGO; GO; 0006687; P: call-call signaling; TAS.

RGO; GO; 0007267; P: call-call signaling; TAS.

RGO; GO; 00001501; P: scall-call signaling; TAS.

RGO; GO; 00001501; P: skeletal development; TAS.

RGO; GO; 00001501; P: skeletal development; TAS.

RGO; GO; GO; PR0001415; Parathyrd hrm.

InterPro; IPR001415; Parathyrd hrm.

PANTHER; PTRR10541; Pchyrhorm_sub.

PANTHER; PTRR10541; Pchyrhorm_sub; 1.

PEam; PF01279; Parathyroid; 1.

PROSORTE; ROSO0335; PRAFINITY.

PROSORTE; PS00335; PRAFINITY.
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C -> R (in FIH; dominant; leads to inefficient processing of the precursor)

FTIG=VAR_006047.
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                                                                                                                                                                                                                                                                                                                          D-structure; Direct protein sequencing; Disease mutation; Hormone;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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-!- FUNCTION: PTH elevates calcium level by dissolving the bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.5%; Score 56; DB 1; Length 115; llarity 91.7%; Pred. No. 0.67; Conservative 1; Mismatches 0; Indels
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12861 MW; 849015736A6E5597 CRC64;
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16-0CT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
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           Ensembl; ENSG0000152266; Homo sapiens.
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115 AA;
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EMBL; X05722; CAA29193.1; -; mRNA.
PIR; B26806; PTPG.
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SEQUENCE 115 AA; 12852 MW;
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TISSUE=PCR rescued clones;
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the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is removed.
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MEDLINE=74253317; PubMed=4840833;

MEDLINE=74253317; PubMed=4840833;

Sader R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,

Potts J.T. Jr.,

"The amino acid sequence of porcine parathyroid hormone.";

"The amino acid sequence of porcine parathyroid hormone.";

Bochemiatry 13:1994-1999(1974).

-I- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.

-I- SUBCELLULAR LOCATION: Secreted.

-I- SIMILARITY: Belongs to the parathyroid hormone family.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukamanlia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
MCBI_TaxID=9823;
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PROTEIN SEQUENCE OF 26-115.
MEDLINE=76018954; PubMed=1164500;
Chu L.L.H., Huang W.-Y., Littledike B.T., Hamilton J.W., Cohn D.V.;
Chordine proparathyroid hormone. Identification, biosynthesis, and partial amino acid sequence.";
Biochemistry 14:3631-3635(1975).
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Pred. No. 0.67;
1; Mismatches 0; Indels
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NUCLECTIDE SEQUENCE.

MEDLINE=87316938, PubMed=3628009,
Schmelzer H.-J., Gross G., Widera G., Mayer H.;
Schmelzer esquence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
By similarity.
By similarity.
By acathyroid hormone.
BC2500EF24BE5597 CRC64;
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PTHY PIG
DT 741Y PIG
STANDARD; PRT; 115 AA.
AC P01269;
DT 21-07L-1986 (Rel. 01, Created)
DT 01-07AY-2005 (Rel. 06, Last sequence update)
DT 10-4AY-2005 (Rel. 47, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                        EMBL, AF130257; AAD42777.1; -; Genomic_DNA.
R HSSP, P01270; 1ET1.
R InterPro; IPR01415; Parathyrd hrm.
InterPro; IPR03625; Pthyrhorm_sub.
PANTHER; PTHH10541; Pthyrhorm_sub.
PERSP; PIRSP01832; PTH; 1.
PROSITE; PS00335; PARTHYROID; 1.
PROSITE; PS00335; PARATHYROID; 1.
HORMONE; Signal.
SIGNAL
SIGNA
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CHAIN 32 115 P
SEQUENCE 115 AA, 12890 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 67.5%;
Local Similarity 91.7%;
es 11; Conservative
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NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

MEDILINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A posters M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Tochkinyki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wickernan K.J., Mallek J.A., Gunber R.D.,

Richards S., Morley K.C., Hale S., Carcia A.M., Gay L.J., Hullyk S.W.,

Prinalon D.K., Wurny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitchigled Y.S.W., Krzywinski M.I., Skalaka U., Smailus D.B.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Buarchontoglires; Primates; Catarrhini; Hominidae;
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67.5%; Score 56; DB 1; Length 115;

Best Local Similarity 91.7%; Pred. No. 0.67;

Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=PCR recound clones;
NIH MGC Project;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases:
EMBL; BC096143; AAH96143.1; -; mRNA.
EMBL; BC096144; AAH96141; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Parathyroid hormone.
9FE8BCDE614BAC16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O4VB48 HUMAN PRELIMINARY, PRT; 115 AA.
O4VB48 (12 SEP-2005 (TEMBLrel. 31, Created)
13 -SEP-2005 (TEMBLrel. 31, Last sequence update)
Parathyroid hormone, preproprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                            Direct protein sequencing; Hormone, Signal SIGNAL
HSSP; P01270; IBWX.
HSSP; P01270; IBWX.
INTERPLO; IPR001415; PRINXHORM_BUD.
INTERPLO; IPR003625; Pthyxhorm_Bub.
PANTHER; PTHX10541; Pthyxhorm_Bub; 1.
PERM; PF01279; PRINXHORG; 1.
PIRSE; PTRSF001832; PTH; 1.
SWART; SMO0187; PTH; 1.
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parathyroid hormone."
Gene 28:319-329(1984)
  NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                              PTHY BOVIN
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                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                    Name=pthl; Synonyms=PTH;
Brachydanio rerio (Zebratish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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0
                                                                                                                            67.5%; Score 56; DB 2; Length 115; 91.7%; Pred. No. 0.67;
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                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            A Constitution of the parathyroid gland.";

"The origin of the parathyroid gland.";

"EMBL, AB176619; BAD72832.1; -; mRNA.

"ZFIN; ZDB-GENE-040623-1; pth1.

"GO; GO:0005176; C:extracellular region; IEA.

"GO; GO:0005179; F:hormone activity; IEA.

"InterPro; IPR001415; Parathyrd hrm.

"InterPro; IPR001415; Parathyrd hrm.

"InterPro; IPR001415; Parathyrd hrm.

"InterPro; IPR001615; Pthyrhorm_sub;

"PAWTHER; PTHR.0541; Pchyrhorm_sub;

"PFGNOPM; PGNIC67; PTH; 1.
EMBL; BC096145; AAH96145.1; -; mRNA.
EMBL; BC096142; AAH96142.1; -; mRNA.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001825; Pthyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
ProDom; PD010687; Pthy. 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
ProDom; PR00135; PTH; 1.
PR081TE; P800135; PARATHYROID; 1.
SEQUENCE 115 AA; 12861 MW; 849015736A6E5597 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 AA; 11641 MW; SAA7B0F8A4110764 CRC64;
                                                                                                                                                                                                                                                                                    01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Parathyroid hormone ligand type-1.
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QSTLZ1;
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Best Local Similarity 83.3°
Eschae 10; Conservative
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Q6WQ25;
                                                                                                                                                       11; Conservative
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                                                                                                                                                                                          Parathyroid hormone.
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                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 Danio.
                                                                                                                                                                                                                                                                                                                                                                                  Cyprinidae; Danio
NCBI_TaxID=7955;
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QG6WQ25 BRA
DG QG6WQ2
AC Q6WQ2
DT 05-JU
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DT 05-JU
DE Parat
GN Brach
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                   A Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
A Bastepe M., Rubin D.A., Uuppner H.;
Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
I Gentification and characterization of two parathyroid hormone-like
I molecules in zebrafish.";
I Endocrinology 145:1634-1639(2004).
EMBL, A2725669; AAQ16566.1; -; mRNA.
EMBL, A2725669; AAQ16566.1; -; mRNA.
EMBL, A2725669; P.Hormone activity; IEA.
GO; GO:0005179; P.Hormone activity; IEA.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001579; Pthyrhorm sub;
R PANTHER; PTHR10541; Pthyrhorm sub;
R Probom; PP01279; Parathyroid; 1.
R Probom; PP01279; Parathyroid; 1.
R Probom; PP01279; PTH; 1.
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MEDLINE=80056617; PubMed=388425;
Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
Potts J.T. Jr., Rich A.,
"Cloning and nucleotide sequence of DNA coding for bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDINES=8426481, PubMed=6086460, DOI=10.1016/0378-1119(84)90149-5;
WEDDINES=8426481, PubMed=6086460, DOI=10.1016/0378-1119(84)90149-5;
WARDLINES-84266481, PubMed=6086460, DOI=10.1016/0378-1119(84)90149-5;
"Isolation and complete nucleotide sequence of the gene for bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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MEDLINE=82037785; PubMed=6170060;
Weaver C.A., Gordon D.F., Kemper B.;
"Introduction by molecular cloning of artifactual inverted seat the 5' terminus of the sense strand of bovine parathyroid at the 5' terminus of the sense strand of bovine parathyroid at the 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.3%; Score 55; DB 2; Length 102; Best Local Similarity 83.3%; Pred. No. 0.84; Matches 10; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11690 MW; SAA7A84FF4110764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MRY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preproparathyroid hormone.";
Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 AA
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NUCLEOTIDE SEQUENCE
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[5]
PROTEIN SEQUENCE OF 26-115.
PROLINE=7414266; PubMed=4522780;
Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T., Jr., Conn D.V.;
The N-terminal amino-acid sequence of bovine proparathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERUCTURE BY NMR OF 32-68.

MEDIATE=20090615; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

MEDIATE=20090615; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;

MEX U.C., Adermann K., Bayer P., Fortsmann W.-G., Rosch P.;

"Solution structures of human parathyroid hormone fragments hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37).";

Blochem. Biophys. Res. Commun. 267:213-220(2000).

-!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.

-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHESIS OF 12-65.

MEDILNE-11091588, PubMed=4122265;

MEDILNE-11091588, PubMed=4122265;

MEDILNE-1-1091588, Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,

METGOS L.J., Dawson B.F., Hogan M.L., Aurbach G.D.,

"Synthesis of a biologically active N-terminal tetratriacontapeptide
of parathyroid hormone.";
                                                                                                                                                                                PROTEIN SEQUENCE OF 32-115.
MEDLINE-71076162; PubMed=5531031;
Mall H.D., Reutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
Aurbach G.D., Potts J.T.,
The amino acid sequence of bovine parathyroid hormone I.";
Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lect protein sequencing; Hormone; Signal.

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6 31
115 Parathyroid hormone
106 V -> G (in 40
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12980 MW; 2ED246B348880710 CRC64;
                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE OF 32-115.
MEDLINE-71063634; PubMed=5275384;
Brewer H.B. Jr., Ronan R.;
"Bovine parathyroid hormone: amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
                                                                                                                                 hormone ";
Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Nat1. Acad. Sci. U.S.A. 68:63-67(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V00106; CAA23439.1; -; mRNA.
EMBL; J000024; AAA30747.1; -; mRNA.
EMBL; K01938; AAA30749.1; -; Genomic_DNA.
EMBL; M25082; AAA30749.1; -; mRNA.
PIR, R24949; PTBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; 1PR001415; Parathyrd_hrm.
InterPro; 1PR001415; Parathyrd_hrm.
InterPro; 1PR001415; Parathyrdorm_sub.
PANTHER, PTHR10541; Pchyrhorm_sub.
Pfam; PF01279; Parathyroid; 1.
PrSP; PRSP001832; PTH; 1.
ProDom; PD010687; Pthyrincm_sub; 1.
PROSTIE; PR00187; PTH; 1.
PROSTIE; PR001835; PANTHROID; 1.
PROSTIE; PR001835; PARATHROID; 1.
DPOSTIE; PR001835; PARATHROID; 1.
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115 AA;
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                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Name-PTH;
Gallus gallus (Chicken).
Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.", 2 Bone Miner Res 3:869-698(1988).

- !- BUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.

- SUBCELULAR COCATION: Secreted.
- !- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE.
MEDLINE=89219100; PubMed=2710135;
Russell J., Sherwood L.M.;
"Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone mRNA and the deduced sequence of the h
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=99284968; PubMed=1251402;
KChosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
Kronenberg H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 1; Length 119; Pred. No. 2.1;
Score 55, DB 1; Length 115;
Pred. No. 0.96;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parathyroid hormone.
B309D8E772997F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMB1, M16604; AAA49093.1; -; mRNA.
EMB1, M36522; AAB02866.1; -; mRNA.
PIR; A34937; A34937.
HSSP, P01270; 1FVY.
Ensemb1; ENSGALG0000005358; Gallus gallus.
InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR00366; PTH related.
InterPro; IPR03825; Pthyrhorm sub.
PANTHER, PTHR10541; Pthyrhorm sub.
PERNF; PIRSF001832; PTH; 1.
                                                                                                                                                                                                                                                                                     PRT; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom, PD013225; PTH "Elated; 1. ProDom; PD013225; PTH "Elated; 1. SMART; SM00087; PTH; 1. PROSITE; PS00335; PARATHYROID; 1. Hormone; Signal. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Endocrinol, 3:325-331(1989).
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: 13943 MW; I
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      Query Match 66.3%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                            1 AVSEIQLMHNLG 12
                                                                                                                                                         32 AVSEIQFMHNLG 43
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
119 AA;
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Best Local Similarity
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NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                           CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.012671499;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of Myperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";
                                                                                                                                                                                                                     Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
"Molecular cloning of feline preproparathyroid hormone.";
"Submitted (OCT-2000) to the BMBL/GenBank/DDBJ databases.
-I- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion (By similarity).
-I- SUBCELULAR LOCATION: Secreted (By similarity).
-I- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                               Felis silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 115;
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By similarity.
Parathyroid hormone.
, 80CD557CC6AlA47E CRC64;
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Last annotation update)
05-JUL-2004 (Rel. 44, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.7%; Score 52; DB 33.3%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001415; Parathyrd hrm.
InterPro; IPR001415; Pthyrhorm_sub.
PANTHER; PTHR10541; Pthyrhorm_sub; 1.
Ptam; PF01279; Parathyroid; 1.
PIRSF; PIRSF001832; PTH; 1.
ProDom; PD010687; Pthyrhorm_sub; 1.
SMART; SM00087; PTH; 1.
PROSITE; PS00335; PANATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
Acetyl_CoA acetyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF309967; AAG30545.1; -; mRNA.
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31 By
115 Pa
12921 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=MK1378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AVSEIQLMHNLG 12
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                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 AA;
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                                                                                                                                         Felinae; Felis.
NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanopyrus
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        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95369696; PubMed=7642102; DOI=10.1016/0378-1119(94)00912-C; Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W., Capen C.C.;
                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequences of the cDNAs encoding canine parathyroid hormone-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 160:241-243(1995).
-!- FUNCTION: PTH elevates calcium level by dissolving the salts in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bone and preventing their renal excretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the parathyroid hormone family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.7%; Score 52; DB 1; Length 115; 83.3%; Pred. No. 2.8; 1; Indels iive 1; Mismatches 1; Indels
        Indels
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By similarity.
Parathyroid hormone.
FC38F77F1C8CFE56 CRC64;
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                                                                                                                                                                                                                         01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-MXY-2005 (Rel. 47, Last annotation update)
Parathyroid hormone precursor (Parathyrin) (PTH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P01268; 1ZWC.
Ensembl; ENSCAFG00000008177; Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 AA
                                                                                                                                                                                     115 AA.
        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR001415; Parathyrd hrm.
InterPro, IPR003625; Pthyrhorm sub.
PANTHER; PTHR10541; Pthyrhorm sub. 1.
Pfam; PF01279; Parathyroid; 1.
PIRSF; PIRSP001832; PTH; 1.
ProDom; PD010687; Pthyrhorm sub; 1.
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                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein and parathyroid hormone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U15662; AAA82584.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 16
PTHY FELCA
ID PTHY FELCA STANDARD;
AC Q9267;
DT 05-JUL-2004 (Rel. 44, Created)
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                                                                    SVSEMQLMHNLG 43
        10; Conservative
                                           1 AVSEIQLMHNLG 12
                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Parathyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hormone; Signal
                                                                                                                                                                                   PTHY CANFA P52212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                             Name=PTH
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01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Novel protein (Fragment)
Name-OTTMUSS00000001188; ORFNames=RP23-5084.2-005;
Mus musculus (Mouse)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Nuridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match S7.8%; Score 48; DB 2; Length 140; Local Similarity 62.5%; Pred. No. 15; les 10; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WICLEOTIDE SEQUENCE.
Phillimore B.;
Phillimore B.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL592065; CAI25664.1; -; Genomic_DNA.
NOW_TER 140
A3 15587 MW; F5108D76C2FFD8EE CRC64;
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OSSXZS MOU
DO SSXZS
MOU
DO SSXZ
DT 01-FE
DT 01-FE
DT 01-FE
DE NOVELL
MARMER
OC BUKAI
OC BUKAI
OC BUKAI
OC MULLIG
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                    Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
EMBL. AE010431; AAM025591.1; -; Genomic_DNA.
GO; GO:0016740; P:transferse activity; IEA.
InterPro; IPR002155; Thiolase.
Pfam; PF02803; Thiolase_C; 1.
Pfam; PF0108; Thiolase_C; 1.
Pfam; PF00108; Thiolase_N; 1.
Scmplete proteome; Transferse.
SEQUENCE 394 AA; 42063 MW; A816CFFFFDE634E4 CRC64;
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EMBL, AAFT01000009; BAL73219.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 885 AA; 97636 MW; 7F56E9DFBC85BEEA CRC64;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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ORFNames=DDB0189350;
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RESULT 19 Q5SXZ6 MOUSE ID Q5SXX6 MOUSE PRELIMINARY; AC Q5SXZ6;

SPIQLIHPNLDSPNVGGGGG 176

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammala, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.

NCBI_TaxID=10090,
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62.5%; Pred. No. 21;
iive 0; Mismatches 6; Indels
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                                                                                                                                                                                 01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Novel protein (Fragment).
Name=CTTMUSP00000001189; ORFNames=RP23-50E4.2-007;
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92 ASKEQQLRHKLGGGSG 107
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QSSXZS;
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US-08-262-495C-4
US-08-691-647C-1
US-08-691-647C-3
US-08-691-647C-3
US-08-691-647C-4
US-08-691-647C-4
US-08-691-647C-4
US-08-904-760B-1
US-08-904-760B-1
US-08-142-551B-56
US-09-730-174A-3
US-09-730-174A-3
US-09-730-174A-9
US-09-730-174A-9
US-09-730-174A-9
US-09-448-867-13
US-09-448-867-13
US-09-448-867-13
US-09-448-867-12
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US-08-904-760B-35
US-09-963-221A-42
US-09-963-221A-42
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/cgn2_6/ptodata1/liaa/RE_COMB.pep:*
/cgn2_6/ptodata1/liaa/Backfiles1.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-421-379-5
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US-10-157-076-9
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US-10-157-076-4
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Sequence 11, Application US/09730174A

Parent No. 6838264

GENERAL INPORMATION:

APPLICANT: Zahradnik, R.J.

ITITE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a

TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hox

FILE REFERENCE: IMUNE-001A

CURRENT APPLICATION NUMBER: US/09/730,174A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12

SEQ ID NO II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
. OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-114A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.1%; Score 59; DB 2; Length 15; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 12; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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Best Local 2; Conservative
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US-09-448-867-5
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Batent No. 6838264

GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HC
FILE REFERENCE: IMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
SEQ ID NOS: 12
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies 0S-09-730-1744-5
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US-09-421-379-5
US-09-421-379-5
i Sequence 5, Application US/09421379
i Patent No. 649562
i GENERAL INFORMATION:
i APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Kronenberg, Henry
APPLICANT: USPREATION:
I TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
ITILE OF INVENTION: Brathyroid Hormone (PTH) and Parathyroid
ITILE OF INVENTION: Hormone-Related Peptide (PTHP)
ITILE OF INVENTION HORMER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
I BARLIER APPLICATION NUMBER: US, 60/105,530
I BARLIER PILING DATE: 1998-10-22
INVENTER PETING DATE: 1998-10-20
INVEN
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, OTHER INFORMATION: Description of Artificial Sequence: synthetic
, OTHER INFORMATION: peptide
US-09-421-379-5
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                                                                                                              ALIGNMENTS
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-730-174A-11
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WESOUL APPLICATION US/09448867

Sequence 5, Application US/09448867

Sequence 5, Application US/09448867

PAPELICANT BRINGHURST, F. RICHARD

APPLICANT: PARASU, HISASHI

APPLICANT: POTTS JR., JOHN T.

TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION

TITLE OF INVENTION: AND USE

TITLE OF INVENTION NUMBER: US/09/448,867

CURRENT APPLICATION NUMBER: US/09/448,867

CURRENT APPLICATION NUMBER: 06/109,938

SARLIER PILING DATE: 1999-11-24

SARLIER PILING DATE: 1999-11-25

NUMBER OF SEQ ID NOS: 13

SSOTID NO 5:

LENGTH: 27
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US-09-448-867-9
| Sequence 9, Application US/09448867
| Sequence 9, Application US/09448867
| Patent No. 6417333
| APPLICANT INFORMATION: A THOMAS J
| APPLICANT GARBELLA, THOMAS J
| TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION J
| TITLE OF INVENTION: AND USE |
| TITLE REPERENCE: 0609-4640001 |
| CURRENT APPLICATION NUMBER: US/09/448,867
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Gaps

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Sequence 9, Application US/10157076

Sequence 9, Application US/10157076

Sequence 9, Application US/10157076

Sequence 9, Application US/10157076

GENERAL INFORMATION:

APPLICANT: Bringhurst, F. Richard

APPLICANT: Takasu, Hisabhi

APPLICANT: Takasu, Hisabhi

APPLICANT: Potts, John T. Jr.

TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use

FILE REFERENCE: 0609-4440002

CURRENT FILING DATE: 1099-112-105

PRIOR FILING DATE: 1999-11-25

PRIOR FILING DATE: 1999-11-25

NUMBER: OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.1

LENGTH: 27
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Sequence 4, Application US/09448867

Patent No. 6417333

GENERAL INPORMATION:

APPLICANT: BRINGHURST, F. RICHARD

APPLICANT: GARDELLA, THOMAS J.

APPLICANT: GARDELLA, THOMAS T.

TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION

TITLE OF INVENTION: HUMAN PARATHYROID

CURRENT FILING DATE: 1999-11-24

EARLIER FILING DATE: 1998-11-25

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 4

LENGTHER PATENTION

LENGTHER PATENTION NOME TO 13

SEQ ID NO 4

LENGTHER PATENTION NOME TO 13

SEQ ID NO 4

LENGTHER PATENTION NOME TO 13
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71.1%; Score 59; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                      Length 27;
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                                                                                                                                                        71.1%; Score 59; DB 2;
100.0%; Pred. No. 0.02;
ive 0; Mismatches
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 27
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Best Local Similarity 100.
Matches 12; Conservative
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ORGANISM: Homo sapiens
                                                                           TYPE: PRT; ORGANISM: Homo sapiens
US-10-157-076-5
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US-10-157-076-9
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APPLICANT: Takasu, Hisashi
APPLICANT: Takasu, Tisashi
APPLICANT: Takasu, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
FILE REFERENCE: 6609-6440002
CURRENT APPLICATION NUMBER: US 09/10/157,076
CURRENT FILING DATE: 2002-05-30
PRIOR FILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-11-25
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Pred. No. 0.02;
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Pred. No. 0.02;
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100.0%; Pred. No. vo...
0; Mismatches
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      CURRENT FILING DATE: 1999-11-24
BARLIER APPLICATION UMBER: 60/109,938
EARLIER FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 13
SEG TWARE: PATENTIN Ver. 2.1
SEQ ID NO 9
LENGTH: 27
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Patent No. 6803213
GENERAL INFORMATION:
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US-09-447-800-7
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-09-448-867-9
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US-09-447-800-7
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MENOUR TO APPLICATION US/10157076

Sequence 8, Application US/10157076

Patent No. 6803213

APPLICANT: Baringhurst, F. Richard

APPLICANT: Takasu, Hissahi

APPLICANT: Gardella, Thomas J.

APPLICANT: Gardella, Thomas J.

APPLICANT: APPLICANT: Gardella, Thomas J.

APPLICANT: Takasu, Hissahi

APPLICANT: Gardella, Thomas J.

APPLICANT: Gardella, Thomas J.

APPLICANT: Gardella, Thomas J.

APPLICANT: Gardella, Thomas J.

PRINTE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use

FILE REFERENCE: 0609-4640002

CURRENT FILING DATE: 2002-05-30

PRIOR FILING DATE: 1999-11-24

PRIOR FILING DATE: 1999-11-25

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Version 3.1

SSO ID NO 8

LENGTH: 28
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1 AVSEIQLMHNLG 12
                                  1 AVSEIQLMHNLG 12
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CRGANISM: Homo sapiens
US-10-157-076-8
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Sequence 4, Application US/10157076

Patent No. 6803213

GENERAL INFORMATION:
APPLICANT: Bringhurst, F. Richard
APPLICANT: Takabu, Hisashi
APPLICANT: Potts, John T. Jr.
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
FILE REFERENCE: 0609.4440002
CURRENT APPLICATION NUMBER: US/10/157,076
CURRENT APPLICATION NUMBER: US 09/448,867
FRIOR FILING DATE: 1999-11-24
FRIOR FILING DATE: 1999-11-25
NUMBER OF SEQ ID NOS: 13
FRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
SEQ ID NO 5
SEQ ID
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US-05-448-867-8

US-05-448-867-8

US-05-448-867-8

Sequence 8, Application US/09448867

Patent No. 641733.

GENERAL INFORMATION:

APPLICANT: TAKASU, HISABIL

APPLICANT: GARDELLA, THOWAS. J

APPLICANT: GARDELLA, THOWAS. J

TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION

TITLE OF INVENTION: AND USE

FILE REPERRNCE: 0609,464,0001

CURRENT APPLICATION NUMBER: 05/99448,867

CURRENT FILING DATE: 1999-11.25

NUMBER OF SEQ ID NOS: 13

SEQ ID NOS: 13

LEAGTH: 28

LENGTH: 28

LENGTH: 28
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                                                  Query Match 71.1%; Score 59; DB 2; Length 28; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 12; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 0
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GRGANISM: Homo sapiens
US-09-448-867-8
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US-10-157-076-4
US-09-448-867-4
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APPLICANT: BRINGHURST, F. RICHARD
APPLICANT: TAKASU, HISBAHI
APPLICANT: TAKASU, HISBAHI
APPLICANT: GARDELLA, THOMAS J.
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMINO-TERMINACGS
FILE REFERENCE: 0609-4630001
CURRENT FILING DATE: 1999-11-23
EARLIER PILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE PARENTIN VOY: 2.1
SEQ ID NO 6
LENGTH: 33
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71.1%; Score 59; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 12; Conservative 0; Mismatches 0; Indels
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; Sequence 3. Application US/08488105
; Patent No. 5717062
; GENERAL INFORMATION:
; APPLICANT: Chorev, Michael
; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHIP
; TITLE OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
; CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE: MA
COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,105
FLING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTOREY/AGENT INFORMATION:
MAME: TESO, Y. ROCKY
REGISTRATION NUMBER: 34,053
REGISTRATION INFORMATION:
TELECHONE: 617/542-8906
TELECHONE: 617/542-8906
TOWNS ATTOREY/AGENT NUMBER: US/08/48/11201
                                                 Sequence 6, Application US/09447800 Patent No. 6537965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD_RES
LOCATION: (1)
CTHER INFORMATION: Desamino Ala
US-09-447-800-6
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FEATURE:
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                           JS-09-447-800-6
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/note= "This C-terminal amino acid is an amide, i.e., CONH2.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "OTHER"
/note= "The side chains of Lys at position 18 and Asp at
position 22 are linked by an amide bond. "
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                                                                                                                                                             Sequence 31, Application US/09228990

Pacent No. 6472505

GENERAL INFORMATION:
APPLICANT: Condon, Stephen M.
APPLICANT: Condon, Stephen M.
APPLICANT: Morize, Isabelle
TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRE-POULEnc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/228,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UDATA:
PRIOR APPLICATION NUMBER: US 60/046,472
FILING DATE: 14-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: MATCIN BQ., Michael B.
REGISTRATION NUMBER: 37,521
REGISTRATION NUMBER: 37,521
REGISTRATION INFORMATION:
TELEPHONE: (610) 454-2793
TELEPHONE: (610) 454-2793
TELEPACK: (610) 454-2793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AVSEIQLMHNLGG 13
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Best Local Similarity 92.3
Matches 12, Conservative
1 AVSEIQLMHNLG 12
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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COTHER INFORMATION:
US-09-228-990-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide
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NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                        RESULT 14
US-09-228-990-31
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The side chains of Lys at position 17 and the side chains of Lys position 13 and Asp at position 30 are linked byy an amide bor position 26 and Asp at position 30 are linked byy an amide bor and this sequence has an amide C-terminus (i.e., COOH).
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US-09-447-800-5
US-09-447-800-5
Sequence 5, Application US/09447800
Patent No. 6537965
GENERAL INFORMATION:
APPLICANT: PARASU, HISASHI
APPLICANT: TARASU, HISASHI
APPLICANT: TARASU, HISASHI
APPLICANT: ARRENTAN: ATHOMAS J.
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
CURRENT APPLICATION NUMBER: US/09/447,800
CURRENT FILING DATE: 1999-11-23
EARLIER APPLICATION NUMBER: 60/110,152
EARLIER PILING DATE: 1998-11-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 71.1%; Score 59; DB 1; Length 34; Best Local Similarity 100.0%; Pred. No. 0.026; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/08408105
Fatent No. 5717062
GENERAL INFORMATION:
APPLICANT: Chorev, Michael
TITLE OF INVERTION:
CORRESPONDENCE CORRESS:
NUMBER OF SEQUENCES: 22
NUMBER OF SEQUENCES: 22
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-488-105-15
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                                                                      RESULT 18
US-08-488-105-15
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                                                                                                                                                  OTHER INFORMATION: The side chains of Lys at OTHER INFORMATION: position 13 and Asp at postion 17 are linked by an amide bond OTHER INFORMATION: and this sequence has an amide C-terminus (i.e., CONH2), rath OTHER INFORMATION: than a carboxy C-terminus (i.e., COCH).
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                                                                                                                                                                                                                                                                                                                                                                                               / March 71.1%; Score 59; DB 1; Length 34; Local Similarity 100.0%; Pred. No. 0.026; Local Similarity 0.00%; Pred. No. 10.00 0.000; Indels of the 12; Conservative 0; Mismatches 0; Indels of the 12 of the 12 of the 12 of the 13 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08488105
| Patent No. 5717062|
| GENERAL INFORMATION: Chorev, Michael APPLICANT: Rosenblatt, Michael TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHEP NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: 7 CORRESPONDENCE ADDRESS: 7 CORRESPONDENCE ADDRESS: 7 STREET: 225 Franklin Street CITY: Boston CITY: Boston COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTE: USA

COMPUTER: TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TAN FC compatible
CURRENT APPLICATION NUMBER: US/08/488,105
FILING DATE: 07-UNN 1995
CLASSIFICATION NUMBER: US/08/488,105
ATTORNEY AGENT INFORMATION:
NAME: TEAL TANTON NUMBER: 34,053
REGISTRATION NUMBER: 00537/112001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH STATE TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
STRANDEDNESS: not relevant
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TELEX: 200154
INFORMATION FOR SEO ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 34 anino acids
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Best Local Similarity 100.
Matches 12; Conservative
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                                 TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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RESULT 20
US-09-843-221A-25
Sequence 25, Application US/09843221A
Sequence 26, Application US/09843221A
Sequence 27, Application US/09843221A
Sequence 27, Application US/09843221A
Sequence 27, Application US/09843221A
APPLICANT: LIU, CHUAN-FA
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: RELATED PROTEIN
TITLE OF INVENTION: ROBER: US/09/843,221A
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/226,673
PRIOR APPLICATION NUMBER: 60/224,860
PRIOR APPLICATION NUMBER: 60/224,860
PRIOR APPLICATION NUMBER: 60/224,860
PRIOR APPLICATION NUMBER: 60/224,860
PRIOR APPLICATION NUMBER: 60/220,053
PRIOR APPLICATION NUMBER: 60/220,053
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71.1%; Score 59; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.1%; Score 59; DB 2; Length 34; Best Local Similarity 100.0%; Pred. No. 0.026; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD_RES
COTATION: (1)
COTHER INFORMATION: Desamino Ala
US-09-447-800-5
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 34
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                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Search completed: November 21, 2005, 16:53:33 Job time : 47 secs (orden) Minora Bood sint

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US-10-998-927-3
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Maximum Match 100%
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RESULT 5

US-10-192-673-5

Sequence 5, Application US/10192673

Sequence 5, Application No. US20030166838A1

GENERAL INFORMATION:

APPLICANT: Gardella, Thomas J.

APPLICANT: MINENTION: Boarding Peptide Derivatives of TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid

TITLE OF INVENTION: Hormone-Related Peptide (PTHP) and Parathyroid

TITLE OF INVENTION: Hormone-Related Peptide (PTHP)

FILE REFERENCE: 0609-457002

CURRENT FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: US. 09/421,379

PRIOR APPLICATION NUMBER: US. 09/421,379

PRIOR APPLICATION NUMBER: US. 00/105,530

PRIOR FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 5

LENGTH: 14

TYPE: PRT
APPLICANT: Hutchison, James Scott
TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
FILE REFREENCE: A1713
CURRENT APPLICATION NUMBER: US/09/898,398
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 13
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US-10-921-368-3

US-10-921-368-3

US-10-921-368-3

Sequence 3, Application US/10921368

Publication No. US20050003493A1

GENERAL INFORMATION:

APPLICANT: Hutchison, James Scott

ITILE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS

FILLE REPERENCE: A1713

CURRENT APPLICATION NUMBER: US/10/921,368

CURRENT FILING DATE: 2004-08-18

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.1

SEQ ID NO 3.3
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                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-898-398-3
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; ORGANISM: Homo sapiens
US-10-921-368-3
                                                                                                                                                                                                                                                            TYPE: PRT
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US-09-730174A-5

US-09-730174A-5

Sequence 5, Application US/09730174A

Patent No. US202020110871A1

Patent No. US202020110871A1

APPLICANT: Zahradnik, R.J.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Ablective Binding Specificity to Bioactive Intact Parathyroid HC CURRENT APPLICATION NUMBER: US/09/730,174A

CURRENT PILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12

LENGTH: 12
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Publication No. US20050095236A1

GENERAL INFORMATION

APPLICANT: Zahradnik, Richard J.

APPLICANT: Lavigne, Jeffrey R.

APPLICANT: Lavigne, Jeffrey R.

TITLE OF INVENTION: Actionacies and Peptide Antigens for Producing Antibodies having in TITLE OF INVENTION: Belective Binding Specificity to Bioactive Intact Parathyroid TITLE OF INVENTION: Hormone (PTH) 1-84

TITLE OF INVENTION: Hormone (PTH) 1-84

CURRENT APPLICATION NUMBER: US/10/998,927

CURRENT PRILING DATE: 2004-11-29

PRIOR PILING DATE: 2000-12-05

NUMBER: PARENT IN NUMBER: US 09/730,174

PRIOR FILING DATE: 2000-12-05

NUMBER: PARENT IN VERSION 3.3

SEQ ID NOS: 12

SEQ ID NOS: 12
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ORGANISM: Artificial Sequence
FEATURE:
CHER INFORMATION: Induces Formation of Antibodies and Isolates Said Antibodies
US-10-998-927-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
... OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-1748-5
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                                                               ALIGNMENTS
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US-09-898-398-3
; Sequence 3, Application US/09898398
; Publication No. US20030082179A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 7, Application US/10361928
; Sequence 7, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HOWAS J.
; TITLE OF INVENTION: ANALOGES
; TITLE OF INVENTION NUMBER: US/10/361,928
; CURRENT FILING DATE: 1099-11-23
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR APPLICATION NUMBER: 60/110,152
; RIGHT FILING DATE: 1999-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
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US-10-484-080-18

Sequence 18 Application US/10484080

Publication No. US20050026839A1

GENERAL INFORMATION:

APPLICANT Cardella, Thomas J.

TITLE OF INVENTION: Hormone (PTH) Analogs

FILE REFERENCE: 6609.5110002

CURRENT FILING DATE: 2004-01-16

PRIOR APPLICATION NUMBER: US/10/484,080

CURRENT FILING DATE: 2002-07-19

PRIOR PILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1

SEOFTWARE: Patentin version 3.1
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 12; Conservat
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Publication No. US20050095236A1

Publication No. US20050095236A1

GENERAL INFORMATION:

APPLICANT: Zahradnik, Richard J.

APPLICANT: Lavigne, Jeffrey R.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Balective Binding Specificity to Bioactive Intact Parathyroid TITLE OF INVENTION: NUMBER: US/10/998,927

CURRENT APPLICATION NUMBER: US 09/730,174

PRIOR PILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.3

SEQ ID NO 11

LENGTH: 15
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APPLICANT: Zahradnik, R.J.
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HG FILE REFERENCE: IMMNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 11
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates Said Antibodies US-10-998-927-11
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                                    ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: peptide
US-10-192-673-5
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                                                                                                                        71.1%; Score 59; DB 4; Length 14; 100.0%; Pred. No. 0.065; tive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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Matches 12; Conservative
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US-10-998-927-11
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US-10-959-605-5
; Sequence 5, Application US/10859605
; Publication No. US20050203012A1
; GENERAL INFORMATION:
; APPLICANT: Bringhuret, F. Richard
APPLICANT: Takasu, Hisashi
APPLICANT: Takasu, Hisashi
APPLICANT: Gardella, Thomas J.
; TITLE OF INVENTION: Huduan Parathyroid Hormone Modifications, Preparation
TITLE OF INVENTION: and Use
FILE REPERENCE: 0609-4640002
; CURRENT APPLICATION NUMBER: US/10/959,605
; CURRENT APPLICATION NUMBER: US/10/157,076
; PRIOR PELICATION NUMBER: US 09/448,867
; PRIOR PELICATION NUMBER: US 09/448,867
; PRIOR PELICATION NUMBER: US 60/109,938
; PRIOR PELICATION NUMBER: US 60/109,938
; SEQUID NO 5
; SEQUID NO 5
; TURIC APPLICATION NUMBER: US 60/109,938
; SOFTWARE: Patentin Version 3.1
; SEQUID NO 5
; TURIC THE CALL OF THE CALL
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US-10-599-605-9
US-10-599-605

1 US-10-599-605

2 Sequence 9, Application US/10959605

3 Publication No. USZ0050203012A1

3 FORBAL INCRMATION:

4 APPLICANT: Taksawi. Hisabhi

A APPLICANT: Taksawi. Hisabhi

A APPLICANT: Gardella, Thomas J.

7 TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation

7 TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation

7 TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation

7 TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation

7 TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation

7 TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation

7 TITLE OF INVENTION UNMERR: US/10/959,605

7 CURRENT FILING DATE: 2004-10-07/10/157,076

7 PRIOR PLILING DATE: 2002-05-30

7 PRIOR PLILING DATE: 1999-11-24

7 PRIOR PLILING DATE: 1999-11-24

7 PRIOR APPLICATION NUMBER: US 60/109,938

7 PRIOR PLILING DATE: 1999-11-25

7 SOFTWARE OF SEO ID NOS: 13

7 SOFTWARE PARENT FILING DATE: 1999-11-25

7 SOFTWARE PARENT FILING DATE: 1999-11-25
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CORGANISM: Homo sapiens
US-10-959-605-9
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US-10-157-076-9
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(WS-10-17-157-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-167-07-
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; ORGANISM: Homo sapiens
US-10-157-076-9
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US-10-157-076-5
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Gaps

1 AVSEIQLMHNLG 12

RESULT 12

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Sequence 8, Application US/10859605

Publication No. US20050203012A1

GENERAL INFORMATION:

APPLICANT: Bringhurst, F. Richard

APPLICANT: Takasu, Hisashi

APPLICANT: Takasu, Hisashi

APPLICANT: Takasu, Hisashi

APPLICANT: Gardella, Thomas J.

APPLICANT: Potts, John T. Jr.

TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation

FILE REFERENCE: 0609-4640002

CURRENT APPLICATION NUMBER: US/10/157,076

PRIOR APPLICATION NUMBER: US 60/109,938

PRIOR APPLICATION NUMBER: US 60/109,938

PRIOR FILING DATE: 1998-11-25

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 8

SEQ ID NO 8

SEQ ID NO 8

SEQ ID NO 8
APPLICANT: Takagu, Hisashi
APPLICANT: Takagu, Hisashi
APPLICANT: Takagu, Hisashi
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation
TITLE OF INVENTION: and Use
FILE REPERENCE: 6069-4640002,
CURRENT APPLICATION NUMBER: US/10/959,605
CURRENT APPLICATION NUMBER: US/10/157,076
PRIOR APPLICATION NUMBER: US 09/448,867
PRIOR APPLICATION NUMBER: US 09/448,867
PRIOR APPLICATION NUMBER: US 60/109,938
PRIOR PILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 28
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US-10-959-605-4
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                Sequence 4, Application US/10157076

Sequence 4, Application US/10157076

Publication No. US20040176568A1

GENERAL INFORMATION:
APPLICANT: Bringhurst, F. Richard
APPLICANT: Takasu, Hisashi
APPLICANT: Takasu, Hisashi
APPLICANT: Takasu, Hisashi
APPLICANT: Potts, John T. Jr.
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
FILE REFERENCE: 0609.4640002

CURRENT APPLICATION NUMBER: US/10/157,076

CURRENT FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: US 60/109,938

PRIOR PILING DATE: 1999-11-25

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENTH: 28
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APPLICANT: Bringhurst, F. Richard
APPLICANT: Takasu, Thomas J.
APPLICANT: Takasu, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Potts, John T. Jr.
TITLE OF INVENTION: Human Parathyroid Hormone Modifications, Preparation and Use
TILE REFERENCE: 0609.4640002
CURRENT APPLICATION NUMBER: US/10/157,076
CURRENT APPLICATION NUMBER: US 09/448,867
PRIOR FILING DATE: 1999-11-25
PRIOR FILING DATE: 1999-11-25
PRIOR FILING DATE: 1999-11-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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Pred. No. 0.13;
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Publication No. US20050203012A1
GENERAL INFORMATION:
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, ORGANISM: Homo sapiens
US-10-157-076-8
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US-10-959-605-4
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Matches

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GENERAL INTEGRALIAL, PAUL
APPLICANT: LOUGEY, DAVID LEE
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE AND PARATHYROID HORMONE APPLICANT: LOUGEY, DAVID LEE
TITLE OF INVENTION: RELATED PROTEIN
FILE REPRENCE: A-665B
CURRENT APPLICATION NUMBER: US/09/843,221A
FILE REPRENCE: 2004-05-04
FRIOR FILING DATE: 2004-05-06
FRIOR FILING DATE: 2000-06-28
FRIOR FILING DATE: 2000-06-28
FRIOR FILING DATE: 2000-06-28
FRIOR FILING DATE: 2000-06-28
FRIOR RELICATION NUMBER: 60/200,063
FRIOR PRILICATION NUMBER: 60/200,063
FRIOR APPLICATION NUMBER: 60/200,063
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Job time : 164 secs
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: rat PTH
US-10-839-037-48
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1 AVSEIQLMHNLG 12
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Publication No. US2
GENERAL INFORMATION
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RESULT 19

RESULT 19

RESULT 19

REQUERICE 48, APDIICATION US/09999608

SEQUENCE 48, APDIICATION US/09999608

SEQUENCE 48, APDIICATION US/0050124537A1

GENERAL INFORMATION:
APPLICANT: KOSTRUIK, PAUL
APPLICANT: JARCSINSKI, MARK ANTHONY
APPLICANT: JARCSINSKI, MARK ANTHONY
APPLICANT: MUNITLER, OLAF BORIS
ITILE OF INVENTION: HORMONE-RELATED PROTEIN
FILE REFERENCE: A-665C
CURRENT APPLICATION NUMBER: US 60/266,673

PRIOR APPLICATION NUMBER: US 60/214,860

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2000-06-28

PRIOR PILING DATE: 2000-04-27

NUMBER OF SEC ID NOS: 193

SEC ID NO 48

SEC ID NO 48

LENGTH: 30
APPLICANT: KOSTENUIK, PAUL

APPLICANT: LLU, CHUANF FA

APPLICANT: LLU, CHUANF FA

APPLICANT: LLU, CHUANF FA

APPLICANT: LLU, CHUANF FA

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H

TITLE OF INVENTION: MELATED PROTEIN

FILE REFERENCE: A-665B

CURRENT APPLICATION NUMBER: US/09/843,221A

CURRENT APPLICATION NUMBER: G0/266,673

PRIOR PELING DATE: 2001-02-06

PRIOR PELING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SOFTWARE PATENTIN NUMBER: 60/200,053

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SSOFTWARE PATENTIN VERSION 3.1

SEQ ID NO 48

LENGTH: 30
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8: /cgn2_6/ptodata/2/pubpaa/US1_NEW_PUB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-939-890-720
US-10-939-890-723
US-10-939-890-353
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Maximum Match 100%
Listing first 100 summaries
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Match Length
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Database

Title: Perfect score:

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831, App 54, App 238, App 30, Appl 48, Appl 3, Appli 20, Appli 3, Appli

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NAME/KEY: MOD_RES

1 LOCATION: (28]...(28)

1 COTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-720
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Song, HO
APPLICANT: Swenson, Kolf E.
APPLICANT: Swenson, Rolf E.
TITLE OF INVENTION: KDR AND VEGFKOR BINDING PEPTIDES
FILE REFERENCE: DO617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR PELING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR PILING DATE: 2003-03-03
PRIOR PELING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-01-15
PRIOR PELING DATE: 2003-03-01
PRIOR FILING DATE: 2003-03-01
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; Sequence 723, Application US/10939890
; Sequence 723, Application US/10939890
; CENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sexton, Daniel J.
; APPLICANT: Ladiner, Robert C.
; APPLICANT: Ladiner, Robert C.
; APPLICANT: Bussat, Christophe
; APPLICANT: Bussat, Christophe
; APPLICANT: Ren, Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                               Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Num, Adrian D.
Arbogast, Christophe
Busast, Philippe
Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SEIQLMHNLGGGGG 16
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          Sequence 6, Appli
Sequence 334, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SONG, BOARDERS, AJSY
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617, 70014US0N D0673
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US/661,156
PRIOR PILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2003-09-13
PRIOR PRILICATION NUMBER: CT/US03/66731
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-01
SPRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NUSER: US 60/360,851
PRIOR FILING DATE: 2003-03-01
      1 US-10-967-648A-6
7 US-11-082-389-334
                                                                                                                      ALIGNMENTS
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(WS-10-939-990-720)
(Schence 720, Application US/10939890)
(Publication No. US20050250700A1)
(GNERAL INFORMATION:
(APPLICANT: Sato, Aaron K.)
(APPLICANT: Saxton, Daniel J.)
(APPLICANT: Dranielield, Daniel T.)
(APPLICANT: Ladner, Robert C.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                                                                                                                                                                             Sequence 464, Application US/10939890 Publication No. US20050250700A1
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                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SEIQLMHNLGGGGG 16
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53.0%; Score 44; DB 1; Length 28;
Best Local Similarity 70.0%; Pred. No. 0.057;
Matches 7; Conservative 1; Mismatches 2; Indels
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APPLICANT: Swenson, Rolf E
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
              CURRENT APPLICATION NUMBER: US/10/939, 890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 353
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CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
NUMBER: OF SEQ ID NOS: 883
SEQ ID NO 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 829, Application US/10939890
Publication No. US20050250700Al
GENERAL INFORMATION:
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Pochon, Sibylle
Ramalingam, Kondareddiar
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Dransfield, Daniel T.
Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
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Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD RES
LOCATION: (28)
COTHER INFORMATION: Lys residue modifed with a SATA linker
US-10-939-890-723
                                                                      APPLICANT: STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT SONG, BO APPLICANT: SWENGON, ROLF E. TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES FILE REFERENCE: DOG/17.7001401800

CURRENT APPLICATION NUMBER: US 10/939,890

CURRENT FILING DATE: 2004-09-13

PRIOR FILING DATE: 2004-09-13

PRIOR FILING DATE: 2003-09-11

PRIOR PELICATION NUMBER: PCT/US03/06731

PRIOR PELICATION NUMBER: US 60/440,411

PRIOR PILING DATE: 2003-03-03

PRIOR FILING DATE: 2003-01-15

PRIOR PILING DATE: 2003-01-15

PRIOR FILING DATE: 2003-01-15

PRIOR PILING DATE: 2003-01-15

PRIOR PILING DATE: 2003-01-15

PRIOR PILING DATE: 2003-01-15

PRIOR OF SEQ ID NOS: 883

SOFTWARE: FREESEQ for Windows Version 4.0

SECTION 0723

LENGTH: 207
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TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 353, Application US/10939890 Publication No. US20050250700Al GENERAL INFORMATION:
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Ladner, Robert C.
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1). (1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SEIOLMHNLGGGGG 16
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Swenson, Rolf E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-939-890-353
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Matches
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Best Local Similarity 53.8%; Pred. No. 0.11; Matches 7; Conservative 4; Mismatches
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14 EVELVDHPGGGG 26
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                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: MOD RES
) LOCATION: (28)
) OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 53.0%; Score 44; DB 1; Length 28; Best Local Similarity 70.0%; Pred. No. 0.057; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%; Score 42; DB 1; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: DG617.70014U0500
CURRENT APPLICATION NUMBER: US/10/919,890
CURRENT FILING DATE: 2004-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PELING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PLILNG DATE: 2003-01-15
PRIOR PLILNG DATE: 2003-01-15
PRIOR PLILNG DATE: 2003-01-15
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PRIOR PLILNG DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
PRIOR PLING DATE: 2003-03-15
PRIOR PLING DATE: 2003-03-15
PRIOR PLING DATE: 2003-03-15
PRIOR PLING DATE: 2003-03-15
PRIOR PLING DATE: 2003-03-03-15
PRIOR PLING DATE: 2003-03-15
PRIOR PLING DATE: 2003-03-1
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Khurana, Sudha
Linder, Karen B.
Marinelli, Edmund R.
Manjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                                         PEATURE:
OTHER INFORMATION: Synthetic peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 354, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
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ORGANISM: Artificial Sequence
                                              TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LMHNLGGGGG 16
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18 MFHQLGGGGG 27
         LENGTH: 28
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (277...(27); OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker US-10-939-890-830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SURGESSON, ROLF E.
APPLICANT: Swenson, Rolf E.
APPLICANT: OND WINDSK!, MATHEW A.
TITLE OF INVENTION: KDR AND VEGFKOR BINDING PEPTIDES
TITLE OF INVENTION: KDR AND VEGFKOR BINDING PEPTIDES
CURRENT FILING DATE: 2004-09-13
CURRENT FILING DATE: 2003-09-11
PRIOR PEPLICATION NUMBER: US 10/661,156
PRIOR PEPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 00/3-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                               Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Manjappan, Palaniappa
Nunn, Adrian D.
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
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Sequence 830, Application US/10939890 Publication No. US20050250700A1 GENERAL INFORMATION:
                                                                                  APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arboqust, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 EIQLMHNLGGGGG 16
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14 EVELVDHPGGGGG 26
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45.8%; Score 38; DB 1; Length 28;
Best Local Similarity 70.0%; Pred. No. 0.48;
Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                          APPLICANT: SWEIGOL, KOLI E.
APPLICANT: SWEIGOL, KOLI E.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.700141800
CURRENT FILING DATE: 2004-09-13
FRIOR APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2003-09-11
FRIOR PILING DATE: 2003-09-11
FRIOR PELING DATE: 2003-09-11
FRIOR PELING DATE: 2003-09-11
FRIOR PELING DATE: 2003-01-15
FRIOR APPLICATION NUMBER: US 60/440,411
FRIOR APPLICATION NUMBER: US 60/400,411
FRIOR APPLICATION NUMBER: US 60/360,851
FRIOR PILING DATE: 2003-01-15
FRIOR PILING DATE: 2003-01-15
FRIOR PILING DATE: 2002-03-01
FRIOR FILING DATE: 2003-01
FRIOR FILING DATE: 2003-03-01
FRIOR FILING DATE: 2003-03-03
FRIOR FILING DATE:
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APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERBENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
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PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Library Isolate US-10-939-890-383
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Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                           Shrivastava, Ajay
                                                                                                                                                                Song, Bo
Swenson, Rolf E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LMHNLGGGGG 16
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18 LNHSPGGGGG 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Song, Bo
APPLICANT: Swengon, Rolf E.
APPLICANT: Swengon, Rolf E.
APPLICANT: Swengon, Rolf E.
APPLICANT: Swengon, Rolf E.
FILE REPERENCE: D0617.70014US00
CURRENT APPLICATION UNDBER: US/10/939, 890
CURRENT FILING DATE: 2004-09-13
PRIOR PTLING DATE: 2003-09-13
PRIOR PTLING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR APPLICATION NUMBER: US 00/306731
PRIOR APPLICATION NUMBER: US 00/440,411
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR APPLICATION NUMBER: US 00/360,851
                                                                                      APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe APPLICANT: Funder, Karen E.
APPLICANT: Hondappan, Palaniappa APPLICANT: Naniappan, Palaniappa APPLICANT: Naniappan, Palaniappa APPLICANT: Naniappan, Palaniappa APPLICANT: Naniappan, Radhakrishna PPLICANT: Pochon, Sibylle PPLICANT: Ramalingam, Kondareddiar PPLICANT: Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-939-890-383
Sequence 383, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
                                                     ; Sequence 346, Application US/10939890; Publication No. US20050250700A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sato, Aaron K.
APPLICANT: Sakcon, Daniel J.
APPLICANT: Sexcon, Daniel J.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe APPLICANT: Bussat, Philippe APPLICANT: Khurana, Sudha APPLICANT: Khurana, Sudha APPLICANT: Linder, Karen E.
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LMHNLGGGGG 16
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18 LNHSPGGGGG 27
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Gaps

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US-10-972-587-37

Sequence 37, Application US/10972587

Publication No. US20050246799A1

Publication No. US20050246799A1

GENERAL INFORMATION:

APPLICANT: Bariola, Pauline Anne
APPLICANT: Fan, Hao

APPLICANT: Fan, Hao

APPLICANT: Fan, Hao

TITLE OF INVENTION: RECEPTORS FOR HYPERSENSITIVE RESPONSE ELICITORS AND

TITLE OF INVENTION: RECEPTORS FOR HYPERSENSITIVE RESPONSE ELICITORS AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 21829/213

CURRENT FILING DATE: 2004-10-25

PRIOR PAPLICATION NUMBER: 00/335,776

PRIOR PELING DATE: 2001-10-31-16

PRIOR PELING DATE: 2001-10-31-6

PRIOR PELING DATE: 2002-06-17

NUMBER OF SEQ ID NOS: 86

SOFTWARE: PatchIIN Ver. 2.1

SEQUENCE: 10 NOS: 86

SEQUENCE: 10 NOS: 86

SEQUENCE: 10 NOS: 86
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                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEX: MD RES
LOCATION: (9) ... (9)
OTHER INFORMATION: Lys residue modified with a iv-Dde linker
FEATURE:
NAME/KEX: MOD RES
LOCATION: (28) ... (28)
COTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-822
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Best Local Similarity 60.0%; Pred. No. 2.4;
Matches 9; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

45.8%; Score 38; DB 1; Length 28;

Best Local Similarity 70.0%; Pred. No. 0.48;

Matches 7; Conservative 1; Mismatches 2; Indels
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US-10-972-587-37
                                                                                                                   FEATURE: OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
105-10-399-890-700
105-10-399-890-700
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105-10-399-890
105-10-39
                                                                                                                                                                     FEATURE:
NAME/KRY: MOD_RES
LOCATION: (1) ...(1)
OTHER_INFORMATION: ACETYLATION
                                                        TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD_RES

1 LOCATION: (28)

1 COTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 45.8%; Score 38; DB 1; Length 28; Best Local Similarity 70.0%; Pred. No. 0.48; Matches 7; Conservative 1; Mismatches 2; Indels
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APPLICANT: SONG; HO
APPLICANT: SONG; HO
APPLICANT: VON WRONGK!, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILLE REPERBENCE: DOG1.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2003-09-13
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR PLING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR PILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FREESEQ for Windows Version 4.0
EDUCTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Abogast, Christophe
APPLICANT: Abogast, Philippe
APPLICANT: Fan, Hong
APPLICANT: Fan, Hong
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Pochon, Sibylle
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 822, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1) -. (1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LMHNLGGGGG 16
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US-10-939-890-822
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APPLICANT: APPLICANT: APPLICANT:

APPLICANT APPLICANT

APPLICANT

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APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M
APPLICANT: Lavalie, Edward R
APPLICANT: Lavalie, Edward R
APPLICANT: Racie, Lisa A
APPLICANT: Racie, Lisa A
APPLICANT: Racie, Lisa A
APPLICANT: Peans, Cheryl
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Wikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TITLE OF INVENTION NUMBER: US/10/689,742
CURRENT FILING DATE: 2000-110-22
PRIOR PAPLICATION NUMBER: 09/746,783
PRIOR PAPLICATION NUMBER: 09/746,783
PRIOR PAPLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PARCENTIN version 3.2
SEQ ID NO 100
LENGTH: 368
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44.6%; Score 37; DB 1; Length 368;
Best Local Similarity 53.8%; Pred. No. 9.7;
Matches 7; Conservative 2; Mismatches 4; Indels
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44.6%; Score 37; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 0.68;
Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                       APPLICANT: SWENGON, KOLT E.
APPLICANT: SWENGON, KOLT E.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REPERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
FRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
FRIOR APPLICATION NUMBER: US 10/382,082
FRIOR FILING DATE: 2003-03-03
FRIOR FILING DATE: 2003-03-03
FRIOR FILING DATE: 2003-03-03
FRIOR FILING DATE: 2003-03-01-15
FRIOR APPLICATION NUMBER: US 60/440,411
FRIOR APPLICATION NUMBER: US 60/360,851
FRIOR APPLICATION NUMBER: US 60/360,851
FRIOR PILING DATE: 2002-03-01
FRIOR FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 100, Application US/10689742
Publication No. US20050250180A1
GENERAL INFORMATION:
                                                                                                                                            Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Library Isolate US-10-939-890-384
Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                           Pillai, Radhakrishna
Pochon, Sibylle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                 Song, Bo
Swenson, Rolf E.
                                                                 Nunn, Adrian D.
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US-10-689-742-100
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APPLICANT:
APPLICANT:
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; NAME/VEY: (27) ... (27)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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85.7%; Pred. No. 0.65;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SDILYABLOAN, ...,
APPLICANT: SONG, BO
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Wan Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.700140500
CURRENT FILING DATE: 2004-09-13
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR PLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR PRIOR DATE: 2003-01-15
PRIOR PLING DATE: 2003-01-15
PRIOR PRIOR DATE: 2003-01-15
PRIOR PLING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 384, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
   Sexton, Daniel J.
Dransfield, Daniel T.
Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
Pan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial sequence
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Khurana, Sudha
Linder, Karen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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20 NVGGGGG 26
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Sequence 9, Application US/11013759;
Sequence 9, Application US/11013759;
Publication No. US20050249747A1
GENERAL INFORMATION:
APPLICANT: Sasaki, Ken
APPLICANT: Sasaki, Ken
APPLICANT: Wang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: BROTEIN OF MORAXELLA
TITLE OF INVENTION: 2004-12-16
CURRENT APPLICATION NUMBER: US/09/361,619
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 9: 32
SEQ ID NO 9: 32
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H.

TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
TITLE OF INVENTION: NOWBER: 1050-013/11/013,759
CURRENT APPLICATION NUMBER: US/09/11/013,759
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR PILLING DATE: 1059-07-27
SOFTWARE: PatentIn Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 7; Length 2047; Pred. No. 1.2e+02; i Mismatches 5; Indels
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; ORGANISM: Moraxella catarrhalis
US-11-013-759-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2047
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US-11-013-759-9
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; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Locemore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Sasaki, Ken
; APPLICANT: Kang, Yan Ping
; APPLICANT: Richi, Michel H.
; TITLE OF INVENTION: RECOMBINANT HICH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: UNMBER: US/11/013,759
; CURRENT APPLICATION NUMBER: US/09/361,619
; RICH REPLEATION NUMBER: US/09/361,619
; RICH RELING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
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Sequence 2. Application US/11169013
Sequence 2. Application No. US20050244971A1
GENERAL INPORMATION:
APPLICANT: Korea Kunho Petrochemical Co., Ltd.
APPLICANT: Korea Kunho Petrochemical Co., Ltd.
TILLE OF INVENTION: TRANSGENIC PLANTS WITH ENHANCED STRESS TOLERANCE:
CURRENT APPLICATION NUMBER: US/11/169,013
CURRENT FILING DATE: 2005-06-29
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Kopatentin 1.71
LENGTH: 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 7; Length 431;
Pred. No. 23;
1; Mismatches 0; Indels
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APPLICANT: Loosmore, Sheena M. APPLICANT: Sasaki, Ken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-169-013-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                  2 VSEIQLMHNLGGG 14
                                                                                   9 HNLGGGG 15
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US-11-013-759-4
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APPLICANT: Marinelli, Edwund R.
APPLICANT: Maniappa, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pochon, Sibyla
APPLICANT: Pochon, Sibyla
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Song, Bo
APPLICANT: Song, Bo
APPLICANT: Song, Mo
APPLICANT: Shrivastava, Ajay
APPLICANT: Shrivastava, Ajay
APPLICANT: Shrivastava, Malay
APPLICANT: Song, Bo
APPLICANT: Won Wromski, Mathew A.
APPLICANT: Won Wromski and Marker and M
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